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A; Accession: JC5917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Riomiey, F.; Binns, M.; Campbell, J.; Boursnell, M.
J. Gen. Virol. 69, 1025-1040, 1988
A;Title: 69, 1026-1040, 1988
A;Title: 69, 1026-1040, 1988
A;Reference number: J70442; MUD:88229622; PMID:2836548
A;Accession: H299653
A;Molecule type: DNA
A;Residues: 1-116 <TOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 1-125 <MAT>
A; Experimental source: snake venom
B; Matsui, T.; Hamako, J.; Suzuki, M.; Hayashi, N.; Ito, M.; Makita, K.; Fujimura, Y.; Oz
Res. Commun. Biochem. Cell Mol. Biol. 1, 271-284, 1997
A; Title: Complete amino acid sequence of bitiscetin, a novel von Willebrand factor modul
A; Reference number: JC5916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y.; 0z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   factor
                                                     60-Val, 61-Lys, 80-Glu, 131-His,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   willebrand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K.; Fujimura,
                                                                                                                                                                                                                                                                  8
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                                                                                                                                                                                                                                                                                                                    75 CPILMTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLITF---PDNQGVKLFGEYLGQDF- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                        131 YWIGLR--NIDG-WRWEGGPALSLRILIN------SLIQRCGAIHR-----NGLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 YWLGASDLNIEGRWLWEGQRRMX---YTNWSPGQPDNAGGIEHCLELRRDLGNYLWNDYQ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSCPILWTRNG----SHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | | : : | | | | | : : : : | | | | | : DIKILYCKEGWVGYNKNCYFFSEEKNNKSLAVERCKDMDGHLTSISSKEEFKFILRYKG 100
                                                                                                                                                                                                                                                                                                                                                          - fowlpox virus (isolate HP-438[Munich])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hepatic lectin homolog (BamHI-ORP8) - fowlpox virus (isolate HP-438[Munich]) C;Species: fowlpox virus C;Species: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jun-2000 C;Accession: H29963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ditiscetin beta chain - puff adder
Ditiscetin beta chain - puff adder
Ditiscetin beta arietans (puff adder)
C;Species: Bitis arrietans (puff adder)
C;Species: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 12-Feb-1999
C;Accession: JC5059; JC5917
R;Matsul, T.; Hamako, J.; Suzuki, M.; Hayashi, N.; Ito, M.; Makita, K.; Fuji
B;Description: Complete amino acid sequence of bitiscetin, a novel von wille
A;Reference number: JC5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: GB:D00295, NID:g221380, PIDN:BAA00203.1, PID:g221394
C;Superfamily: fowlpox virus hepatic lectin homolog, C-type lectin homology
C;Keywords: early protein
F;48-116/Domain: C-type lectin homology #status atypical <LEC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                               29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Score 107.5; DB 1; Length 116;
7; Pred. No. 0.0024;
14; Mismatches 32; Indels 5;
                                                                                                                                                                                                    DB 2; Length 155;
                                                                                                                                                                                                                                                               Indels
                                        A;Note: 4-Pro, 4-IIe, 9-His, 11-Gly, 20-Arg, 45-Asp, 60-Val, C;Superfamily: tetranectin; C-type lectin homology
F;1-155/Product: perlucin #status experimental <MAT>
F;136-155/Region: 10-residue repeats (N/D-S-L-H-A-N-L-Q-Q-R)
                                                                                                                                                                                                 ch 10.6%; Score 109.5; DB 2; Similarity 26.9%; Pred. No. 0.0021; 36; Conservative 21; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 10.4%;
1 Similarity 29.2%;
21; Conservative 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 ASSCEVALQWICKK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---CQKPSHFICEK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 QDFYWIGLRNID 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 PGNHWİĞIEKVD 112
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                                                                                                                                                                                              Query Match
Best Local S:
Matches 36
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Best Local 8
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Matches
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7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ---CFVAESFHN 106
                                                                                                                                                                                                                                                                                                                                      63
                                         A, Experimental source: venom C; Experimental source: venom codulator of a von Willebrand factor modulator. C; Superfamily: tetranectin; C-type lectin homology C; Reywords: venom F; 4-121/Domain: C-type lectin homology <LCH>>
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                          43;
                                                                                                                                                                                                                                                                                    79 WTRNGSHCYYFSMEKKDWNSSLKFCAD--KGSHLLTFPDNQGVKLFGEYLGQ--
                                                                                                                                                                                           DB 2; Length 125;
                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                         10.3%; Score 105.5; DB 2; 24.8%; Pred. No. 0.0042; iive 15; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                              64 VLVWIGLSHF--WRICPLRWTDGARLDYRALSDEPI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: August 10, 2004, 16:44:40
Job time : 14.5 secs
                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KWIQWTCNR 115
A; Molecule type: protein A; Residues: 1-125 < MA2>
                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 32; Conserv
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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sw model - protein search, using protein ĕ

August 10, 2004, 16:36:04; Search time 8 Seconds Run on:

(without alignments) 1223.649 Million cell updates/sec

1 MADSSIYSTLELPEAPQVQD......GLQASSCEVALQWICKKVLY 188 US-09-811-367B-3 1029 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 Scoring table:

BLOSUM62

141681 seqs, 52070155 residues Searched:

40997 Total number of hits satisfying chosen parameters:

length: 0 length: 188 Minimum DB seq Maximum DB seq Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9mzk9 macaca mula	Q13241 homo sapien	Q9mz41 pan troglod					Q92478 homo sapien					P81114 trimeresuru		bothrops j	bothrops			P81113 trimeresuru	_	P23806 trimeresuru	P35230 mus musculu	7	P07439 megabalanus	P81996 echis carin	Q9ygpl trimeresuru	Q06141 homo sapien		P81508 crotalus ho	P81112 trimeresuru	P21963 crotalus at	P42854 rattus norv	P25031 rattus norv
SUMMARIES	ID	CD94 MACMU	CD94 HUMAN	CD94 PANTR	IXB TRIFL	CVXE CRODU	V239 FOWPV	MMHB AGKHA	CLE2_HUMAN	MMHA AGKHA	VOO8 FOWPV	RHCA AGKRH	CHBB_CROHO	ABA4 TRIAB	CVXA CRODU	BOTA_BOTJA	BOTE BOTJA	PLC HALLA	RHCB AGKRH		PAP3_MOUSE	IXA_TRIFL	PAP1 MOUSE	PAP2_MOUSE	LEC3_MEGRO	ECHB ECHCA	LECG_TRIST	PAP1 HUMAN	LITH RAT	CHBA CROHO	ABA2_TRIAB	LECG_CROAT		PAP1_RAT
	DB	Н	Н	 4	Н	Н	н	Н	Н	ч	Н	Н					Н	Н	Н	Н	۲	Н	Н	Н	Н	Н	1	Н					Н	Н
	Query Match Length	179	179	179	146	148	163	146	149	157	167	133	117	123	158	133	125	155	129	125	174	152	175	175	162	123	158	175	165	127	134	135	174	175
940	Query Match		17.3	•	•	14.6	14.2	14.1	14.0	3	ы	2	2	12.1	Н	11.6	11.0	10.7	10.6	10.5	10.2	10.1	10.0	10.0	10.0	6.6	6.6	9.6	9.5	4.6	9.4		9.5	9.1
	Score	180.5	178.5	178.5	152.5	150.5	146.5	145	144	139	138	125.5	124.5	124.5	120.5	119	113.5	110.5	109.5	108.5	105	104	103	103	102.5	101.5	101.5	101	97.5	97	97	97	95	94
	Result No.	7	7	٣	4	S	9	7	æ	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

EMBL; AF190931; AAF74527.1; -. EMBL; AF190932; AAF74528.1; -.

P81116 trimeresuru Q95mil pan troglod	P05140 hemitripter 043908 homo sapien	Q92778 mesocricetu P05451 homo sapien	P48304 homo sapien P81017 echis carin	Q9psn0 bitis ariet Q9psm4 lachesis st	P23132 bos taurus P81115 trimeresuru
ABBB_TRIAB NKGF_PANTR	ANP HEMAM NKGF HUMAN	PBCG_MESAU LITA_HUMAN	LITB_HUMAN ECHA_ECHCA	LECG_BITAR LECG_LACST	LITH_BOVIN ABBA_TRIAB
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118	163	175	166	135 135	175
و و ۲. و	0.8	8.8	8.7	8 8 4 4	8 8 4 6.
93.5	93	91	89.5	8 6 8 6	85.5
3.4 5.5	36	38 39	40 41	42 43	4 4 5

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21158386; PubMed=11261935; Kravitz R.H., Grendell R.L., Slukvin I.I., Golos T.G.; Sravitz R.H., Grendell R.L., Slukvin I.I., Golos T.G.; Spiression of NKG2-A and NKG2-C mRNAs and novel alternative splicing of 5' exons in rhesus monkey decidua."; Immunogenetics 53:69-73(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                ú
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells. -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
                                                        Q9MZK9; Q9GK91; Q9MZK7; Q9MZK8; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Natural killer cells antigen CD94 (NK cell receptor) (Killer cell lectin-like receptor subfamily D, member 1).
                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                              [1]

SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).

MEDLINE=20322487; PubMed=10866118;

LaBonte M.L., Levy D.B., Letvin N.L.;

"Characterization of rhesus monkey CD94/NKG2 family members and identification of novel transmembrane-deleted forms of NKG2-A, B, and D.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          members.
-!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event-Alternative splicing; Named isoforms=3;
Name=1; Synonyms=CD94-A;
Isold=O9MXK9-1; Sequence=Displayed;
Name=2; Synonyms=CD94-B;
Isold=O9MXK9-2; Sequence=VSP_003055;
Name=3; Synonyms=CD94 alt;
Name=3; Synonyms=CD94 alt;
Isold=O9MXX9-3; Sequence=VSP_033054;
--- TISSUE SPECIFICITY; Natural killer cells.
                                      179 AA.
                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenetics 51:496-499(2000).
                                                                                                                                                                                                         Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                           NCBI_TaxID=9544;
                                                                                                                                                                                       KLRD1 OR CD94.
                                         MACMU
RESULT 1
CD94_MACMU
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us-09-811-367b-3.closed.rsp

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EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
  85 HCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID---GW 141
                                                                                                                                                                                                                                                                                                                                                                                              71 NCYFISSEEKTWNESRHFCASQKSSLLQLQNRDELDFMSS--SQHFYWIGLSYSEEHTAW 128
                                                                                                                                                                                                                                                                                                                                                     70
                             InterPro; IPR001304; Lectin_C.
Pfam; PF000059; lectin_c; 1.
SMART; SM00034; CIECT, 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS00641; C_TYPE_LECTIN_2; 1.
Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin; Alternative splicing; Polymorphism.
                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL).
MAVFKTTLWRLISGTLGIICLSLMATLGILLKNS -> MAA
                                                                                                                                                                                                                                                                                                                                   ----KDSTCSHCPSCPILWTRNGS
                                                                                                                                                                                                                                                                                                                                                     14 GTLGIICLSLMATLGILLKNSFTKLSVEPAYTPGPNIELQKDSDC--C-SCHEKWVGYRC
                                                                                                    CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Blood;
MEDLINE=96011848; PubMed=7589107;
Chang C., Rodriguez A., Carretero M., Lopez-Botet M., Phillips J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD94 HUMAN STANDARD, PRT; 179 AA.
Q13241; O43321; O43773; Q9UBE3; Q9UEQ0;
O1-NOV-1997 (Rel. 35, Careaed)
O1-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 44, Last annotation update)
Natural killer cells antigen CD94 (Nx cell receptor)
Hectin-like receptor subfamily D, member 1) (KP43).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                             31;
                                                                                                                                                     BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                    142 RWEGGPALSLRILTNSLI---QRCGAIHRNG-LQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                               129 IWENGSALSQYLFPSFETFKPKNCIAYNSKGNALDESCETKNRYICKQQL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rodriguez A., Carretero M., Glienke J., Bellon T., Ramirez A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular characterization of human CD94: a type II membrane glycoprotein related to the C-type lectin superfamily."; Eur. J. Immunol. 25:2433-2437(1995).
                                                                                                                                                                                                                                                                                          ch 17.5%; Score 180.5; DB 1; Length 179; I Similarity 31.8%; Pred. No. 6e-11; 54; Conservative 17; Mismatches 68; Indels 31
                                                                                                                                                                                                                                                                      06212B4494527F07 CRC64;
                                                                                                                                  EXTRACELLULAR (POTENTIAL)
C-TYPE LECTIN (LONG FORM)
BY SIMILARITY.
                                                                                                                                                                                                                                       (In isoform 2).
                                                                                                                                                                                                                                                 FTIG=VSP_003055.
                                                                                                                                                                                                                             FTIG=VSP 003054.
                                                                                                                                                                                                                     in isoform
                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                  44 GLLTVILMSLLMYQRILCCGS------
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MEDLINE=98139529; PubMed=9472066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                      20607 MW;
EMBL; AF190933; AAF74529.1;
EMBL; AF294886; AAG34498.1;
HSSP; P22897; 1EGG.
                                                                                                   10
                                                                                                                                                                                                                                         105
                                                                                                                                  179
176
72
174
166
83
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                                                                                                                                                                                                                                                                      179 AA;
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                        105
                                                                                                                                  32
98
61
89
152
132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLRD1 OR CD94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lanier L.L.;
                                                                                                                                                      DISULFID
                                                                                                                                                                         DISULFID
CARBOHYD
CARBOHYD
                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                       VARSPLIC
                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                             VARIANT
                                                                                                                                  DOMAIN
                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD94 HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
KINDLINE=22388257; PubMed=12477932;
Karausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Batcow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
A batchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Poshiyuki S., Carninci P., Prange C.,
Raha S.B., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muxny D.M., Madan A., Rodrigues S., Sanchez A.,
Mitting M., Madan A., Young A.C., Shevohenko Y., Bouffard G.G.,
Blakesley R.M., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Mara M.A.;
Human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 3).
MEDLINE=98267245; PubMed=9601951;
Furukawa H., Yabe T., Watanabe K., Miyamoto R., Akaza T., Tadokoro K., Tohma S., Inoue T., Yamamoto K., Juji T.;
"A alternatively spliced from of the human CD94 gene.";
Immunogenetics 48:87-88(1998).
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-!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
-!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- SUBCECLULAR LOCATION: Type II membrane protein.
-!- ALTERMATIVE PRODUCTS:
BVENT-Alternative splicing; Named isoforms=3;
Name=1; Synonyms=CD94-A;
ISOId=Q13241-1; Sequence=Displayed;
Name=2; Synonyms=CD94-B;
ISOId=Q13241-1; Sequence=VSP_00363;
Name=3; Synonyms=CD94-B;
ISOId=Q13241-3; Sequence=VSP_00362;
-!- TISSUB SPECIFICITY: Natural killer cells.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
-!- DATABASE: NAME=PROW; NOTE=CD guide CD94 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd94.htm".
                                                                                                                                                                                                                                                                 Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
Lehrach H., Francis F., Lopez-Botet M.; "Structure of the human CD94 C-Type lectin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y14287; CAA74663.1; -.
Y14288; CAA74663.1; JOINED.
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                                                                                       Immunogenetics 47:305-309(1998)
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EMBL; AB009597; BAA24450.1; -
EMBL; AB010084; BAA24451.1; -
EMBL; BC028009; AAH28009.1; -
PDB; 1B6E; 15-JUN-99.
                                                                                                                                                                                   (ISOFORM 2)
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                                                                                                                                                                              SEQUENCE FROM N.A.
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Matches
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IXB_TRIFL
                                                                                                                         NKG2
SOLUTION STATEMENT OF STATEMENT
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                  MIM; 602894; -.

R MIM; 602894; -.

R GO; GO:0005886; C:plasma membrane; TAS.

GO; GO:0005886; P:transmembrane receptor activity; TAS.

BR GO; GO:0005960; P:antimicrobial humoral response (sensu Inver...; TAS.)

BR GO; GO:0007166; P:cell surface receptor linked signal transdu...; TAS.

BR GO; GO:0007166; P:cell surface receptor linked signal transdu...; TAS.

BR GO; GO:0007166; P:cell surface receptor linked signal transdu...; TAS.

BR GO; GO:0007166; P:cell surface receptor linked signal transdu...; TAS.

BR GO; GO:0007166; P:cell surface receptor linked signal transdu...; TAS.

BR GO; GO:0007166; P:cell surface receptor linked signal transdu...; TAS.

BR GO; GO:0007166; P:cell surface receptor linked signal transdu...; TAS.

BR GO; GO:0007166; P:cell surface receptor linked signal transdu...; TAS.

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BR GO; GO:0007166; P:cell surface receptor linked signal transdur...; TAS.

BR GO; GO:0007166; P:cell surface receptor linked signal transdur...; TAS.

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BR GO; GO:0007166; P:cell surface receptor linked signal transdur...; TAS.

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BR GO; GO:0007166; P:cell surface receptor linked signal transdur...; TAS.

BR GO; GO:0007166; P:Cell surface receptor linked signal transdur...; TAS.

BR GO; GO:0007166; P:Cell surface receptor linked signal transdur...; TAS.

BR GO; GO:0007166; P:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID---GW 141
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MAVFKTTLWRLISGTLGIICLSLMATLGILLKNS -> MAA
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28-FEB-2003 (Rel. 41, Last sequence update)
10-CT-2003 (Rel. 42, Last annotation update)
Natural killer cells antigen CD94 (NK cell receptor) (Killer cell
lectin-like receptor subfamily D, member 1).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELULAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GACNAC. ..) (POTENTIAL).
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Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L.,
Muir D.G., Canavez F., Cooper S.L., Vallante N.M., Lanier L.L.,
Parham P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 RWEGGPALSLRILTN---SLIQRCGAIHRNG-LQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LWENGSALSQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQQL 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 9.5e-11;
; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1884D99E8D9583A7 CRC64;
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/FTId=VSP 003053
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MEDLINE=21623889; PubMed=11751968;
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Genew; HGNC:6378; KLRD1
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98
61
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DISULFID
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VARSPLIC
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 HCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID---GW 141
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InterPro; IERG1304; Lectin_C.
PHan; PF00059; lectin_c; 1.
PROSITE; P800615; C_TYPE_LECTIN_I; PALSE_NEG.
PROSITE; P850041; C_TYPE_LECTIN_I; PALSE_NEG.
Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin; Alternative splicing and antigen.
DOMAIN.

100 CVMANT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL)
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                              -!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I., Cleland S., Guethlein L.A., Uhrberg M., Parham P.; "Conservation and variation in human and common chimpanzee CD94 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLONAC. .) (POTENTIAL).
N-LINKED (GLONAC. .) (POTENTIAL).
L -> LQ (in isoform 2).
/FTIG=VSP_003056.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.3%; Score 178.5; DB 1; Length 179; 31.8%; Pred. No. 9.5e-11; ive 17; Mismatches 68; Indels 31.
                                                                                                                                                                                                                                                                                                                                  Name=1; Synonyms=CD94-A;
IsoId=Q9WZ41-1; Sequence=Displayed;
Name=2; Synonyms=CD94-B;
IsoId=Q9WZ41-2; Sequence=VSP 003056;
TISSUS SPECIFICITY: Natural killer cells.
SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7244D99E8D9587E7 CRC64;
                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- ALTERNATIVE PRODUCTS:
EVent-=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ą.
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P23807; Q91247;
01-NOV-1991 (Rel. 20, Created)
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                                                                                                        J. Immunol. 168:240-252 (2002)
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98
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CVXB CRODU
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97331317; PubMed=9187649; Mizuno H., Atoda H., Morita T.; Mizuno H., Fujimoto Z., Koizumi M., Kano H., Atoda H., Morita T.; Mizuno H., Pujimoto Z., Koizumi M., Kano H., Atoda H., Morita T.; of C-type lectin domains."; 15 Miz. Struct. Biol. 4:438-44. (1997).

-I Struct. Biol. 4:438-44. (1997).

-I FUNCTION: Anticoagulant protein which binds with factor IX and factor X in the presence of calcium with a 1 to 1 stoichiometry.

-I SUBUNIT: Heterodimer of chains A and B; disulfide-linked.

-I SUBCELLULAR LOCATION: Secreted.

-I MISCELLANBOUS: Calcium is required for ligand binding.

-I SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=96184662; PubMed=8645314;
MEDLINE=96184662; PubMed=8645314;
Matsuzaki R., Yoshihara B., Yamada M., Shima K., Atoda H., Morita T.;
Matsuzaki R., Yoshihara B., Yamada M., Shima K., Atoda H., Morita T.;
"cDNA, cloning of IX/X-BP, a heterogeneous two-chain anticoagulant
"cDNA, cloning of IX/X-BP, a heterogeneous two-chain anticoagulant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COAGULATION FACTOR IX/FACTOR X-BINDING
                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Eppidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea; Viperidae, Crotalinae, Trimeresurus.
                                                                                                                                                                                                                                                                                         AEDLINE-91332000, PubMed=1831197, Atoda H., Hyuga M., Morita T.;
Athe primary structure of coagulation factor IX/factor X-binding protein isolated from the venom of Trimeresurus flavoviridis. Homology with asialoglycoprotein receptors, proteoglycan core protein, tetranectin, and lymphocyte Fc epsilon receptor for
15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Coagulation factor IX/factor X-binding protein B chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (WITH C-102 IN A CHAIN).
BY SIMILARITY.
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PDB; ILXX; 06-MAX-98.
PDB; ILXX; 06-MAX-98.
INTERPRO; IPR001304; Lectin_C.
INTERPRO; IPR001309; Pancreatis_ac.
INTERPRO; IPR01509; Pancreatis_ac.
PRINTS; PR01504; PRCFEATITISAP.
SWART; SW00034; CLECT; 1.
PROSITE; PS000615; C_TYPE_LECTIN_1; 1.
PROSITE; PS000615; C_TYPE_LECTIN_2; 1.
Lectin; Calcium; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem. 266:14903-14911(1991).
                                                             Trimeresurus flavoviridis (Habu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D83332; BAA11888.1; -.
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446
446
446
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444
                                                                                                                                                                                                                                                                   SEQUENCE OF 24-146.
                                                                                                                                                                                                                                                                                                                                                                                         immunoglobulin E.";
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                                                                                                                                                                                                                                                                                                                                                                                                                      95 DWNSSLKFCADK--GSHLLTFPDNQG----VKLFGEYLGQDFYWIGLRNI---DGWRWEG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SLSGTAADCPSD---WSSYEGHCYKPFSEPK 44
                                                                                                                                                                                                                                                                                                                                                   35 LSRFAMVALGLITVILMSLLMYQRILCCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKK
                                                                                                                                                                                                                                                                                                                      25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Crotalus durissus terrificus (South American rattlesnake).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leduc M., Bon C.;
"Cloning of subunits of convulxin, a collagen-like platelet-
aggregating protein from Crotalus durissus terrificus venom.";
Biochem. J. 333:389-393(1998).
                                                                                                                                                                                                                                                                                    Length 146;
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SEQUENCE FROM N.A., AND SEQUENCE OF 24-53; 99-109 AND 126-145.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                     16922 MW; 8E1961C59F96757C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 GPALSLRILINSLIQRCGAIHRNGLQASSCEVALQWICK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 AAMLRYKAWAEESYCVYFKSTNNKWRSRACRMMAOFVCE 143
                                                                                                                                                                                                                                                                                    14.8%; Score 152.5; DB 1; 24.5%; Pred, No. 3.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                      25; Mismatches
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InterPro; IPR003990; Pancreatis_ac.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Venom gland;
MEDLINE=98324901; PubMed=9657980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viperidae, Crotalinae, Crotalus
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HSSP; P23807; 11XX.
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146 AA;
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30; GO:0005576; C:extracellular; IC.
EMBL; D00295; BAA00203.1;
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                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DWNSSLKFCADK--GSHLLTFPDNQG----VKLFGEYLGQDFYWIGLRNI---DGWRWEG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47 TWADAEKFCTQQHTGSHLVSFHSTEEVDFVVKMTHQSLKSTFFWIGANNIWNKCNWQWSD 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : || |: || |: || |: :| | :: || :: || |: :| | |: :| || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 LSRFAMVALGLLTVILMSLLMYQRILCCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-116 FROM N.A.
STRAIN=FP-9 / Isolate HP-438;
MEDLINE=88229622; PubMed=2836548;
MEDLINE=88229622; PubMed=2836548;
"Squence analysis of an 11.2 kilobase, near-terminal, BamHI fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fowlpox virus (FPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                INTERCHAIN (WITH C-158 IN ALPHA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                  INTERCHAIN (WITH C-104 IN ALPHA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Afonso C.L., Tulman B.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.; "The genome of fowlpox virus."; J. Virol. 74:3815-3831(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 4.9e-08; his matches 42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fowlpox virus.";
Gen. Virol. 69:1025-1040(1988).
- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY,
94D7E3E1BC693B9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V239_FOWPV STANDARD; PRT; 163 AA.
P14371; Q9J500;
01-JAN-1990 (Rel. 13, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Putative C-type lectin protein FPV239 (BamHI-ORF8).
                                                                                                                                                                                                           CONVULXIN BETA.
                                                                                                                                                                                                                                                                                                                       BY SIMILARITY. BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.6%; Score 150.5;
                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
         PRINTS; PRO1504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN 1; 1.
PROSITE; PS0041; C_TYPE_LECTIN 2; 1.
Lectin; Glycoprotein; Signal.
33 GNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20193820; PubMed=10729156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF198100; AAF44583.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17402 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ilarity 31.4%;
Conservative 1
Pfam; PF00059; lectin c; 1.
                                                                                                                                                                                                     148
145
26
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                                                                                                                                                                                                                                                                                                                                                                               100
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148 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Avipoxvirus.
NCBI_TaxID=10261;
                                                                                                                                                                                                                                                                                                                    27
55
100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FPV239.
                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 PSCPILWTRNG----SHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNOGVKLFGEYLG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 ODFYWIGLRNID---GWRWEGGPALSLRILINSLIORCGAIHRNGLQASSCEVALQWICK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 PGNEWIGIEKVDFNGTWKLEDGSSYD-NIVPIKGIGDCAYLSDRSIMSSFCFLPKKWICR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sakurai Y., Fujimura Y., Kokubo T., Imamura K., Kawasaki T., Handa M., Suzuki M., Matsui T., Titani K., Yoshioka A.;
"The cDNA cloning and molecular characterization of a snake venom platelet glycoprotein Ib-binding protein, mamushigin, from Agkistrodon halys bromhoffii venom.";
Thromb. Haemost. 79:1199-1207(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thromb. Haemost. 79:1199-1207(1998).
-!- FUNCTION: Binds to platelet glycoprotein Ib and enhances platelet aggregation at low-shear stress. At high-shear stress, aggregation is inhibited.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDIKILYCKEGWVGYNKNCYFFSEEKNNKSLAVERCKDMDGHLTSISSKEEFKFILRYKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., SEQUENCE OF 24-56, SUBUNIT, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agkistrodon halys blomĥoffi (Manushi) (Gloydius blomhoffii).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBCELLULAR LOCATION: Secreted.
-!- MASS SPECTROMETRY: NW=15413; NW_ERR=6; METHOD=Electrospray;
                                                                                                                                                                                                                                                                                                                                                                              Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: Heterodimer of alpha and beta chains; disulfide-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                            C-TYPE LECTIN.
5156DC8928855532 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 57;
                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                              14.2%; Score 146.5; DB 1
26.8%; Pred. No. 1.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Mamushigin beta chain precursor.
PIR; H29963; WMVZFB.

HSSP; P05140; ZAFP.
InterPro; IRR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
PROSITE; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viperidae; Crotalinae; Gloydius
NCBI_TaxID=242054;
                                                                                                                                                                                                                                                                                                           18635 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB019616; BAA34425.1; -.
                                                                                                                                                                                                                                        Hypothetical protein; Lectin. DOMAIN 48 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                               163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P23807; 1IXX.
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RANGE=24-146.
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                           89
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                                                                                                                                                                                                                                                                                    95 DWNSSLKFCAD--KGSHLLTFPDNQG----VKLFGEYLGQDFYWIGLRNIDGW-----RW 143
                                                                                                                                                                                                                                                                                                   45 TWEDAEKFCTQQRKESHLVSFHSSEEVDFVVSMTWPILKYDFVWIGLINII--WNECHVJEW 102
                                                                                                                                                                                                                                        35 LSRFAMVALGLITVILMSLLMYQRILCCGSKDSTCSHCPSCPILMTRNGSHCYYFSMEKK 94
                                                                                                                                                                                                                                                               --SLSGTGADCPSD---WSSYEGHCYRVFQKEM 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDILNE=99173880; PubMed=10072769;
Yokoyama-Kobayashi M., Yamaguchi T., Sekine S., Kato S.,
"Selection of CDNAs encoding putative type II membrane proteins on the cell surface from a human full-length cDNA bank.",
                                                                                                                                                                                                                                                                                                                                                                                                              CLE2_HUMAN STANDARD; PRT; 149 AA.
092478; 098478; 091644;
28-FEB-2003 (Rel. 41, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
C-type lectin superfamily member 2 (Activation-induced C-type lectin).
CLESP2 OR AICL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21388257; PubMed-12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Maruslina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hamann J., Montgomery K.T., Lau S., Kucherlapati R., van Lier R.A.W., "AICL, a new activation induced antigen encoded by the human NK gene
                                                                                                                                                                                                                     Gaps
                                                                                                                                      INTERCHAIN (WITH C-103 IN ALPHA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                      48;
                                                                                                                                                                                              Length 146;
                                                                                                                                                                                                                                                                                                                                                 144 EGGPALSLRILTNSLIORCGAIHRNGLQASSCEVAL----QWICK 184
                                                                                                                                                                                                                      55; Indels
                                                                                                                                                                         9EDA84BDCC24E76D CRC64;
                                                                                          MAMUSHIGIN BETA CHAIN.
                                                                                                                                                                                              Score 145; DB 1;
Pred. No. 1.7e-07;
                                                                                                                                                 (BY SIMILARITY).
BY SIMILARITY.
                                                                                                     C-TYPE LECTIN.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                    17; Mismatches
                                                                                                                          SIMILARITY
GO:0007596; P:blood coagulation; IDA
         InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS000615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Blood coagulation; Lectin; Signal.
                                                                                                                                                                                                                                                      MEDLINE=97190245; PubMed=9038101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mmunogenetics 45:295-300(1997).
                                                                                                                                                                      17064 MW;
                                                                                                                                                                                           14.18;
27.38;
                                                                                                                                                                                                                    45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Urinary bladder;
                                                                                         146
143
36
142
98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene 228:161-167(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                      146 AA;
                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        103 TDGTRLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complex."
                                                                                                                                    DISULFID
                                                                                                                                                            DISULFID
                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                             Query Match
                                                                             SIGNAL
                                                                                                     DOMAIN
                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                      CLE2_HUMAN
                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 KDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGL---RNIDGWRWEGGPALS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO:0005530; F:lectīn; TAS. GO:0006960; F:antimicrobial humoral response (sensu Inver. . .; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 HLSRFAMVALGLITVILMSLLMYQRILCCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEK 93
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.D., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Schwerzer S.W., Schmutz J., Myers R.W., Schmutz J., Skalska U., Samilus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 HKKCFIIVGV-LITTNIITLIVKL----TRDSQ----SLCPYDWIGFONKCYYFSKEE
                                                                                                                                                                                                                                                                                                                    tissues,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                    Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 LRILINSLIQR----CGAIHRNGLQASSCEVALQWICKKVLY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 ---FTKSFGMRGSEGCAYLSDDGAATARCYTERKWICRKRIH 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0B4FED23424F6C55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C-TYPE LECTIN.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . . ) (IN LINKED (GLCNAC. . . ) (IN LINKED (GLCNAC. . ) (IN LINKED (GLCNAC. . ) (IN REF. 1) . . . . T (IN REF. 1) . . . . . . H (IN REF. 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB015628; BAA76495.1; -.
EMBL; BC005254; AAH05254.1; -.
EMBL; BC005254; AAH05254.2; -.
EMBL; BC005342; -.
GO; GO:0005887; C:integral to plasma membrane; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Transmembrane; Lectin; Signal-anchor.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.0%; Score 144; DB 1; 26.5%; Pred. No. 2.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.5%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001304; Lectin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17307 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00059; lectin c; 1. SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X96719; CAA65480.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
100
100
107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
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145
63
144
136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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442
442
123
123
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 KWADAERRCTEGRITGAHLVSIESNTBAAFVNQMISENIKKTDYVWIGLTVQNEEQQCKSR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DWNSSLKFCADK--GSHLLTFPDNQGVKLFGEYLGQ-----DFYWIGL--RNIDGW---R 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 LSRFAMVALGLLTVILMSLLMYQRILCGGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGRFIFVSFGLL-VVFLSL-----SGAEDDS-----DCPSDWSSNGRFCYKLFQQKM 46
                                                                                                                                                                                                                                                                                                       platelet glycoprotein Ib-binding protein, mamushigin, from Agkistrodon halys bromhoffii venom.";
Thromb. Haemost, 79:1199-1207(1998).
                                                                                                                                                                                                                                                                                                                                                Thromb. Haemost. 79:1199-1207(1998).
-!- FUNCTION: Binds to platelet glycoprotein Ib and enhances platelet aggregation at low-shear stress. At high-shear stress, aggregation is inhibited.
                                                                                                                                                                                                       SEQUENCE FROM N.A., SEQUENCE OF 22-58, SUBUNIT, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERCHAIN (WITH C-98 IN BETA CHAIN) (BY
                                                                                                                                                                                                                                                        Sakurai Y., Fujimura Y., Kokubo T., Imamura K., Kawasaki T., Handa
Suzuki M., Matsui T., Titani K., Yoshioka A.;
"The cDNA cloning and molecular characterization of a snake venom
                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Gloydius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULLAR LOCATION: Secreted.
MASS SPECTROMETRY: MW-16825; MW_ERR=2.7; METHOD=Electrospray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26;
                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: Heterodimer of alpha and beta chains; disulfide
                                                                                  Mamushigin alpha chain precursor.
Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RANGE=22-157.
SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        // SIMILARITY.
47DAA17891CE1865 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAMUSHIGIN ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 139; DB 1;
Pred. No. 7.4e-07;
26; Mismatches 51;
                             10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
157 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C-TYPE LECTIN.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005576; C:extracellular; IC.
GO; GO:0007596; P:blood coagulation; IDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY)
BY SIMILARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00615; C_TYPE_LECTIN 1; 1. PROSITE; PS50041; C_TYPE_LECTIN_2; 1. Blood coagulation; Lectin; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis ac.
                                                                                                                                                                                                                                           MEDLINE=98319530; PubMed=9657448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00059; lectin_c; l.
PRINTS; PR01504; PNCREATITSAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB019615; BAA34424.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18333 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.5%;
26.4%;
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SM00034; CLECT; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157
152
38
151
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157 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P23806; 11XX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blood coagulation;
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                            TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37;
MIMHA AGKHA
                                                                                                                                                                                                                                                                                                                                                                                                                                         linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 DWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGL---RNIDGWRW-----EGG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 LSRFAMVALGLLTVILMSLLMYQRILCCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEXK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 VSCYALITULGILCILLETILV---VVTCKMYYAFPYFSKVCPDEWIGYNSKCYYFTINET
                                                                                                                                                                                                                                                                                                                                                                                Tomley F., Binns M., Campbell J., Boursnell M.E.G.,
"Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment
                                                                                                                                                                                                                                                             Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDIJNE=20193820; PubMed=10729156;
Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock
"The genome of fowlpox virus.";
J. Virol. 74:3815-3831(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 167;
                                                                                                                                                                          01-JAN-1990 (Rel. 13, Last sequence update)
8-FFBE-2003 (Rel. 41, Last annotation update)
Putative C-type lectin protein FPV008/FPV253 (BamHI-ORF2)
FPV008 AND FPV253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C769ECAABAD238ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.4%; Score 138; DB 1; 27.1%; Pred. No. 1e-06; iive 28; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FIRE DESCRIPTION OF THE PROPERTY OF THE PROPERTY SMOODS; LECTIN C; 1.

SMART; SMOODS; LECTIN C; 1.

SMART; SMOODS; C TYPE LECTIN 1; FALSE NEG. PROSITE; PSSOO41; C TYPE LECTIN 2; 1.
                                                                                                                         167 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C-TYPE LECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=88229622; PubMed=2836548;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gen. Virol. 69:1025-1040(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 PALSLRILTNSLIQRCGAIH 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 NDICLLFDTSNIIEMSCIFH 147
143 WEGGPALSLRILTNSLIQRC 162
                               107 WSDRSSVSYENLVKPNSKKC 126
                                                                                                                                                          01-JAN-1990 (Rel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF198100; AAF44607.1; -. EMBL; AF198100; AAF44608.1; -. PIR; B29963; WMVZF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19869 MW;
                                                                                                                                                                                                                                                                                                                                                     Isolate HP-438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D00295; BAA00192.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38; Conservative
                                                                                                                         STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             fowlpox virus.";
                                                                                                                                                                                                                                                Fowlpox virus (FPV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10261;
                                                                                                                                                                                                                                                                                     Avipoxvirus
                                                                                                                                                                                                                                                                                                                                                       STRAIN=FP-9
                                                                                                                         FOWPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                       P14370
                                                                                                      FOWPV
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TISSUE=Venom;
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P81114;
              SEOUENCE
                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                    Lectin.
                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 NKIYRSWIGLKIENKGQRSNLE---WSDGSSISYENLYEPYMEKCFLMDHQSGLPKMHTA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Rhodocetin alpha subunit.
Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CPILWTRNGSHCYYFSMEKKDWNSSLKFCA--DKGSHLLTFPDNQGVKLFGEYLGQDFY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----WIGLR-----NIDGWRWEGGPALSLRILTWSLIQRCGAI-HRNGL---QAS
                                                                                                                                                                                                          venom of
                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SINILARITY: Contains 1 C-type lectin family domain.
-!- SINILARITY: Contains 1 C-type lectin family domain.
HSPP: P23806; 11XX.
InterPro; IPR001304; Lectin C.
FFam; PR00053; lectin c; 1.
SMART; SM00034; CLECT, 1.
PROSITE; PS00615; C_TYPE_LECTIN 1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                            noncovalent interaction therefore it is subunits.";
Biochemistry 38:7584-7593(1999).
-!- FUNCTION: A potent inhibitor of collagen-induced platelet aggregation. Individually, neither subunit inhibits platelet aggregation. Both subunits are essential.
-!- SUBUNIT: Heterodimer of one alpha and one beta subunit held together by noncovalent interactions rather than by intersubunit disulfide bridges.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                           Eŭkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Calloselasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scieroglossa, Serpentes, Colubroidea,
Viperidae, Crocalinae, Crotalus.
NCBI_TaxID=8747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 133;
                                                                                                                                                                                          Wang R., Kini R.M., Chung M.C.M.; "Rhodocetin, a novel platelet aggregation inhibitor from the Calloselasma rhodostoma (Malayan pit viper): synergistic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LONG FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / SIMILARITY.
386EAC519DFC674D CRC64;
                                                                                                                                                       SEQUENCE, FUNCTION, SUBUNIT, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Last annotation update)
CHH-B beta subunit.
Crotalus horridus horridus (Timber rattlesnake).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     C-TYPE LECTIN (;
BY SIMILARITY,
BY SIMILARITY.
            133 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 125.5;
Pred. No. 1.4
           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                               MEDLINE=99303998; PubMed=10360956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΒY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
                                  (Rel. 36, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15962 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.2%;
26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34; Conservative
           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | | :: | |
118 DCEEKNVFMCK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 SCEVALQWICK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                       129
13
127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                   NCBI_TaxID=8717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      30
102
                                                                                                                                                                     TISSUE=Venom;
                                  15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P81509;
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Lectin.
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                     P81397
RHCA AGKRH
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MEDLINE=96420502; PubMed=8823201;
Andrews R.K., Kroll M.H., Ward C.M., Rose J.W., Scarborough R.M.,
Andrews R.K., Kroll M.H., Ward C.M., Rose J.W., Scarborough R.M.,
Smith A.I., Lopez J.A., Berndt M.C.,
The smith and related viper venom proteins to the platelet membrane albolabris and related viper venom proteins to the platelet membrane glycoprotein ID-T-X complex. Effect on platelet aggregation and to glycoprotein ID-mediated platelet activation.";
Elochemistry 35:12629-12639(1996).
I. FUNCTION: Binds to platelet GPIB/IX receptor system, inhibits VWF binding, and stimulates agglutination.
I. SUBUNIT: Heterodimer of alpha and beta subunits; disulfide-linked.
I. SUBCELIULAR LOCATION: Secreted.
I. SUBCELIULAR LOCATION: Screted.
II. SIMILARITY: Contains 1 C-type lectin family domain.
InterPro; IPR001253; AntifreezeII.
R. InterPro; IPR001254; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 CPILWTRNGSHCYYFSMEKKDWNSSLKFCADK--GSHLLTFPDNQGVKLFGEYLGQDFYW 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 IGLRNIDGW-----RWEGGPALSLRILT---NSLIQRCGAIHRNGLQASSCEVALQWICK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Binds to platelet GPlb/IX receptor system and stimulates agglutination.
SUBUNIT: Heterotetramer of the subunits 1, 2, 3 and 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 CPSDWSSYEGHCYRVFQQEMTWDDAEKFCTQQHTGGHLVSFRSSEEVDFLVSILKFDLFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERCHAIN (WITH C-81 IN ALPHA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Alboaggreejin A subunit 4.
Trimeresurus albolabris (White-lipped pit viper).
Trimeresurus Albolabris (White-lipped pit viper).
Lepidosauria; Squamata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crocalinae; Trimeresurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98189535; PubMed=9531050; Rowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J., Calvete J.J., Niewiarowski S., "Alboaggregins A and B. Structure and interaction with human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disulfide-linked.
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07835BBCB61E9EAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.1%; Score 124.5; DB 1
25.8%; Pred. No. 1.5e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-TYPE LECTIN.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00615; C TYPE LECTIN 1; PROSITE; PS50041; C TYPE LECTIN 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79:609-613 (1998)
                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00059; lectin c; 1.
PRINTS; PR00356; ANTIFREEZEII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13888 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00034; CLECT; 1
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13
115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            platelets.";
Thromb. Haemost.
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BOTA BOTJA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 CPILWTRNGSHCYYFSMEKKDWNSSLKFCAD--KGSHLLTFPDNQG----VKLFGEYLGQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 DFYWIGLRNIDGW-----RWEGGPALSLRILINSLIQRCGAIHRNGLQASSCEVALQWIC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NLVWIGLSNL - - WNQCNSQWSDGTXLDYKXWREQFECLVSRTTNNEWLSMDCSSTHSFVC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 24-48; 61-68; 108-120; 139-145 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crotalus durissus terrificus (South American rattlesnake).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Crotalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aggregating protein from Crotalus durissus terrificus venom.";
Biochem. J. 333:389-393(1998).
-!- FUNCTION: Binds to the platelet and collagen receptor,
glycoprotein VI (GPVI).
-!- SUBUNIT: HeteroPhexamer of three alpha chains and three beta chains; disulfide-linked.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leduc M., Bon C.;
"Cloning of subunits of convulxin, a collagen-like platelet-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                             C-TYPE LECTIN (LONG FORM)
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         D4CFBEE1219C9B1E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Pred. No. 1.6e-05; 18; Mismatches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last amotation update)
Convulxin alpha precursor (CVX alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 124.5;
                                                                                                                                                                                                  PROSITE, PS00615; C TYPE LECTIN 1; 1.
PROSITE, PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPK001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
Pfam; PF00059; lectin_c; 1.
                             InterPro; IPR002353; AntifreezeII.
InterPro; IPR001304; Lectin_C.
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MEDLINE=98324901; PubMed=9657980;
                                                                                                   Pfam; PF00059; lectin c; l. PRINTS; PR00356; ANTIFREEZEII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         14365 MW;
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25.6%;
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nes 31; Conservative
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   HSSP; P23807; 11XX.
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COVXA, CRODU
LD 28-FEB-
DT 28-FEB-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ONKEKQCSTKWSDGSSVSYDNLLDLYITKCSLLKKKHTGFRKWFVASCIGKIPFVCK 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GWRWEGGPALSIRILINSLIQRCGAIHR-NGLQ---ASSCEVALQWICK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Venom,
MEDLINE=91129280; PubMed=1993206;
Pujimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T.,
Fuki H., Sugimoto M., Ruggeri Z.M.;
"Isolation and chemical haracterization of two structurally and
functionally distinct forms of botrocetin, the platelet coagglutinin
isolated from the venom of Bothrops jararaca.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Primary structure of two-chain botrocetin, a von Willebrand factor modulator purified from the venom of Bothrops jararaca.";
Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).
                                                                                                                           C-TYPE LECTIN.
BY SIMILARITY.
SY SIMILARITY.
INTERCHAIN (WITH C-100 IN BETA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Structural basis of von Willebrand factor activation by the snake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bothrops jararāca (Jararaca).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Guamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
                                                                                                                                                                                                                                       INTERCHAIN (WITH C-26 IÑ BETA CHAIN)
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Fukuda K., Doggett T.A., Bankston L.A., Cruz M.A., Diacovo T.G.,
                                                                                                                                                                                                                                                                                                                                               49;
                                                                                                                                                                                                                                                                                                           Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93157385; PubMed=8430107;
Usami Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui
                                                                                                                                                                                                                                                                                                                                               57; Indels
                                                                                                                                                                                                                                                    (POTENTIAL).
949F9C6D673E2318 CRC64;
                                                                                                                                                                                                                                                                                                             DB 1;
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01-JUL-1993 (Rel. 26, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Botrocetin, alpha chain (Platelet coagglutinin).
                                                                                                                                                                                                                                                                                                         11.7%; Score 120.5; DB 1
25.0%; Pred. No. 5.3e-05;
PRINTS; FRUIDOUS; CLECT; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C TYPE_LECTIN 1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                              26; Mismatches
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                                                                                                                                                                                                                                                                         158 AA; 18141 MW;
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47 NWEDAEWFCTKQAKGAHLVS-
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nes 44; Conservative
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                                                                                  VWF, and the complex then bridge to precent

To platelet agglutination.

To platelet agglutination.

To platelet agglutination.

The dimeric form is factor-dependent platelet coagglutinin. The dimeric form is a 34-times more active than the one-chain botrocetin in promoting vWF binding to platelets.

To vWF binding to platelets.

To subtrocetin and vWF form a soluble complex.

To subtrocetin and vWF form a solu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 -----QDFY-WIGLR--NID---GWRWEGGPALSLRILTNSLIQRCGAIHRN 168
Structure 10:943-950(2002).
-!- FUNCTION: Two-chain botrocetin forms an activated complex with vWF, and the complex then binds to platelet GPIb, resulting in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERCHAIN (WITH C-75 IN BETA CHAIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 11.6%; Score 119; DB 1; Length 133; Best Local Similarity 25.4%; Pred. No. 6.2e-05; Matches 29; Conservative 26; Mismatches 33; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 120
133 AA; 15215 MW; B4CF4502946AC74B CRC64;
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Search completed: August 10, 2004, 16:42:47 Job time : 9 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 10, 2004, 16:39:05; Search time 32 Seconds (without alignments) 1853.669 Million cell updates/sec Run on:

US-09-811-367B-3

1029 1 MADSSIYSTLELPEAPQVQD......GLQASSCEVALQWICKKVLY 188 Sequence:

Perfect score:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1017041 seqs, 315518202 residues

Searched:

Total number of hits satisfying chosen parameters:

396094

Minimum DB seq length: 0 Maximum DB seq length: 188

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

SPTREMBL 25:*

sp_archea:*

sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_mhc:*
sp_organelle:* vertebrate:* unclassified:* bacteriap:* sp_bacteria:*
sp_fungi:*
sp_human:* sp_rodent:*
sp_virus:* rvirus:* sp_plant:* sp phage:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:

		Description	088713 mus musculu	Q64335 rattus norv	054708 mus musculu	O54707 mus musculu	Овщиув ропао руаша	Osmija pongo pygma	O8mhy9 pongo pygma	OBmii4 pongo pygma	O9nzsl homo sapien	Osspx0 sus scrofa	O9r007 mus musculu	OgiamO aqkistrodon	08jiw1 agkistrodon	095194 bos taurus	09qlf4 sus scrofa	Q8r4k5 rattus norv
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SUMMARIES		ID	088713	064335	054708	054707	Q8MHY8	Q8MJI3	Q8MHY9	Q8MJI4	Q9NZS1	Q8SPX0	Q9R007	Q9IAM0	QBJIW1	Q95JG4	Q9GLF4	Q8R4K5
		DB	11	11	11	11	9	9	9	9	4	9	11	13	13	9	9	11
		Match Length DB	188	188	179	179	179	179	179	179	181	159	165	146	146	161	165	132
	% Query	Match	100.0	81.4	17.5	17.5	17.2	17.0	17.0	16.7	16.7	16.4	16.3	15.9	15.9	15.8	15.6	15.5
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MGD; MGI:1355294; Klrgl.

Q8b124 mus musculu Q8aya4 agkistrodon Q9gK90 macaca mula Q8av98 trimeresuru Q35778 rattus norv	Q9glf3 sus scrofa Q81gt6 trimeresuru Q8wup7 homo sapien Q91840 ackistrodon	Q71045 vipera lebe Q9mzj6 macaca mula Q8mkJ4 pongo pygma Q9hd37 homo sanien	Q9dg31 agkistrodon Q8uvc7 agkistrodon Q9ny25 homo sapien	QBaya3 agkistrodon Q9deal agkistrodon Q9ygn4 agkistrodon QBmjh4 pongo pygma QBmjh3 pongo pygma	Q91zw9 mus musculu Q95j54 pan troglod Q8jiv7 agkistrodon O9ukq0 homo sanien	Q8uvc6 agkistrodon Q8ayas agkistrodon Q9def8 agkistrodon Q8cj86 mus musculu
Q8BL24 Q8AYA4 Q9GK90 Q8AV98 Q35778	Q9GLF3 Q8JGT6 Q8WUP7 O9T840	Q7T045 Q9MZJ6 Q8MHY4 09HD37	Q9DG31 Q8UVC7 Q9NY25	QBAYA3 Q9DEA1 Q9YGN4 Q8MJH4 Q8MJH3	Q91ZW9 Q95J54 Q8JIV7 O9UKO0	Q8UVC6 Q8AYA5 Q9DEF8 Q8CJ86
11 13 13 11	13	6 6 6 4	13	13 13 6	11 6. 13	13 13 11
164 146 163 148	185 146 154	146 185 162 173	146 149 188	1449 1446 145 162	178 183 146 187	158 158 146 142
15.5 15.2 15.2 14.9	14.6	4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	14.0 14.0	13.9 13.8 13.6 13.5	13.5 13.5 13.4	13.3 13.3 13.2 13.1
159.5 158.5 156 154 154	150 148.5 148 146.5	146.5 145.5 145	144.5 144 143.5	141.5 141.5 140 139	138.5 137.5 137.5	136.5 136.5 135.5 135
17 18 19 20 21	2 2 2 2 2 2 4 2 2 2 4 2 2 2 2 2 2 2 2 2	25 27 28 29	30 31 32	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	38 8 6 7 4 10 0 1	4 4 4 4 2 6 4 5

ALIGNMENTS

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SEQUENCE FROM N.A.

STRAIN=C.B-17 SCID;

MEDLINBES9077194; PubMed=9862378;

Hanke T., Corral L., Vance R.E., Raulet D.H.;

"2Fl antigen, the mouse homolog of the rat '$1', is a lectin-like type II transmembrane receptor expressed by natural killer cells.";

Eur. J. Immunol. 28:4409-4417(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=129/SvevTACfBr; TISSUB=Spleen;
MEDLINE=2111316; PubMed=1122062;
Voebringer D., Kaufmann M., Pircher H.;
"Genomic structure, alternative splicing, and physical mapping of the killer cell lectin-like receptor G1 gene (KLRG1), the mouse homologue
                                                                                                                                                                                                  01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Mast cell function-associated antigen 2F1 (MAFA) (Killer cell lectin-like receptor G1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                            188 AA.
                                                                                                                                                                           01-NOV-1998 (TrEMBLrel. 08, Created)
                                                                                            PRT;
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EMBL, AP097357, AAD03718.1; -.
EMBL, AJ010751, CAA0343.1; -.
EMBL, AF317727, AAX40082.1; -.
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                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                KLRG1 OR MAFA.
Mus musculus (Mouse).
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                                                                                                                            61 CCGSKGFMCSQCSRCFNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN
                                                                                                                                                                                                              1 MADNSIYSTLELPAAAPRVQDDSRWKVKAVLHRPCVSYLVWVALGLLTVILMSLLLYQRTL
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                   MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 SRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRILCCGSKDST
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Vance R.E., Tanamachi D.M., Hanke T., Raulet D.H.;
"Cloning of a mouse homolog of CD94 extends the family lectins on murine natural killer cells.";
Eur. J. Immunol. 27:3236-3241(1997).
EMBL, AF030312; AAC28244.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20809 MW; D59E1CBB63139E45 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last sequence update)
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SMARY; SM0034; CLECT; l.
PROSITE; PS50041; C_TYPE_LECTIN_2; l.
PROSITE; PS00022; EGF l; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1196275; Klrdl.
GO; GO:0005529; F:Rusgar binding; IEA.
InterPro; IPR006209; EGF like.
InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 06, (TrEMBLrel. 06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                         WICKKVL 187
                                                                                                                                                                                                                                                                                                     181 WICEKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CB.17 SCID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLRD1 OR CD94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998
01-JUN-1998
                                                                                                         61
                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     054707;
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054707
                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
054708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96016176; PubMed=7568140;
A Guthmann M.D., Tal M., Pecht I.;
"A secretion inhibitory signal transduction molecule on mast cells is
"A secretion inhibitory signal transduction molecule on mast cells is
"A secretion inhibitory signal transduction molecule on mast cells is
"A secretion inhibitory signal transduction molecule on mast cells is
"A secretion inhibitory signal transduction molecule on mast cells is
"A secretion inhibitory signal transduction molecule on mast cells is
mother C-type lectin.";

Proc. Natl. Acad. Sci. U.S.A. 92:9397-9401(1995).

BRBL; X97192; CAA65829.1; JOINED.
BRBL; X97194; CAA65829.1; JOINED.
BRBL; X97194; CAA65829.1; JOINED.
BRBL; X79912; CAA65829.1; JOINED.
BRBL; X79912; CAA65829.1; JOINED.
BR PIR; I59421; I59421.

R PIR; I59421; I59421.

R PIR; I59421; LEGTIN.

R PIRM; PF00059; lectin.C.

R SMART; SM0034; CLECT; I.

R SMART; SM0034; CLECT; I.
                                                                                                                                                                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LFGEYLGQDFYWIGLRNIDGWRWEGGPALSLRILTNSLIQRCGAIHRNGLQASSCEVALQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                     61 CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120
                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                      1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL
                                                                                                                                                                                                                                                                                                                                                                                  CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 LFGEYLGQDFYWIGLRNIDGWRWEGGPALSLRILINSLIQRCGAIHRNGLQASSCEVALQ
                                                                                                                                                                                                                                                                                               1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                11; Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.4%; Score 838; DB 11; Length 1
80.7%; Pred. No. 1.5e-79;
ive 15; Mismatches 21; Indels
                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-SPRAGUE DAWLEY, TISSUB=Testis;
STRAIN-SPRAGUE DAWLEY, TISSUB=Testis;
BOOCK Jr P. (Athhmann M.D., Pecht I.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS50041; C_TYPE_LECTIN_2; 1.
188 AA; _21356 MW; \(\bar{2}\)CC8032D4D020B15 CRC64;
                                                                                                                                                                    188 AA; 21396 MW; 876336802EA134F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:000529; F:sugar binding; IEA.
GO; GO:0007157; P:heterophilic cell adhesion; IEA.
InterPro; IPR001304; Lectin_C;
FAM, PF00059; lectin_C; 1...
SMARY; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_Z; 1.
                                                                                                                                                                                                           100.0%; Score 1029; DB 11;
100.0%; Pred. No. 1.5e-99;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q64335,
01-NOV-1996 (TrEMBLrel. 01, '01.NOV-1996 (TrEMBLrel. 01, '01.-0.T-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 81.4'
Best Local Similarity 80.7'
Matches 151; Conservative
                                                                                                                                                                                                                                                     188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WICKKVLY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WICKKVLY 188
                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                Lectin; Receptor
SEQUENCE 188 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAFA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
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                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   064335
                                                                                                                                                                                                                                                     Matches
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9

Gaps

62

m

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SEQUENCE FROM N.A.

MEDLINE-2072192; DubMed=12077248;

MEDLINE-2072192; DubMed=12077248;

Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;

"NK Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors with MHC-C. "19:220-229(2002).

"With MHC-C." "19:220-229(2002).

"MEDL, AF470384; AAM78484.1; -..

R GO, GO:0004872; F:receptor activity; IEA.

"GO, GO:0004872; F:receptor activity; IEA.

"R GO, GO:0004872; F:sugar binding; IEA.

"InterPro; IPR001304; Lecfin.C.

"InterPro; IPR001304; Lectin.C.

"R Pfam; PF00059; lectin.C.; 1...

"R SMART; SM00034; CLECT7.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 HCYYPSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID---GW 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 NCYFISSEQKTWNESRHLCASQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEEHTAW 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guethlein L.A., Flodin L.R., Adams E.J., Parham P.; "NK Cell Receptors of the Oranguean (Pongo pygmaeus): A Pivotal Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors with MHC-C.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pongo pygmaeus (Orangutan).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 RWEGGPALS---LRILINSLIQRCGAIHRNG-LQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 LWENGSALSQYLFPLFETFNPKNCIAYNPNGNALDESCEDKNRYICKQQL 178
                                                                                                                                                                                                                                                                                                                                                   17.2%; Score 177.5; DB 6; Length 179; 31.8%; Pred. No. 1.7e-10; Live 16; Mismatches 69; Indels 31
                                                                                                                                                                                                                                                                                                                  179 AA; 20550 MW; 6752CB8F182CFD73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 AA; 20566 MW; 6752CB8F0F9A2609 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.0%; Score 174.5; DB 6;
31.2%; Pred. No. 3.4e-10;
tive 17; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ā
                                                                                                                                      GO, GO:0004872; F:receptor activity; IEA, GO, GO:0005529; F:sugar binding; IEA. InterPro; IPR00509; EGF like.
                                                                                                                                                                                                                Pfam, PF00059; lectin_c; 1.7
SMART; SM00034; CLET; 1.
PROSITE; PS00041; C TYPE LECTIN_2; 1.
PROSITE; PS00022; EGF_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE, PS50041; C_TYPE_LECTIN_2; 1. PROSITE; PS00022; BGF_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 GLLTVILMSLLMYQRILCCGS----
                                                                              J. Immunol. 169:220-229(2002).
EMBL; AF470381; AAM78481.1; -.
EMBL; AF470382; AAM78482.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                 44 GLLTVILMSLLMYORILCCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Natural killer cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                         54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POPY-CD94.
                                                                                                                                                                                                                                                                                                Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUÊNCE
                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8MJI3
                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 ILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGGYLGQDFYWIGL- 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 DKWVGHQCNCYFISKEEKSWKRSRDFCASQNSSLLQ-PQSRNELSFWNF-SQTFFWIGMH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----CSHCPSCP 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----RNIDGWRWEGGPALSLRILTN-SLIQRCGAI---HRNGLQASSCEVALQWICKKV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRWRLMSVIFGIK-CLFLMVTLG---VLLINSFTIQNIQSTPSPTTTVEFQEVSECCVCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CS7BL/67; TISSUE=Mammary gland;
Butcher S., Cottage A., Cook G.P.;
"Mouse natural killer cell receptors homologous to human CD94 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                      STRAIN=CS7BL/6J;
Heusel J.W., Ho E.L., Brown M.G., Matsumoto K., Yokoyama W.M.;
"Murine CD94.";
01-OCT-2003 (TrBMBLrel. 25, Last annotation update)
Killer cell lectin-like receptor, subfamily D, member 1 (CD94)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 SRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRILCCGSKDST-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC-1997) to the BMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 AA; 20808 MW; DD343419E93B3465 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                          STRAIN=CS7BL/6;
Vance R.E., Tanamachi D.M., Hanke T., Raulet D.H.;
Eur. J. Immunol. 27:0-0(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1196275; Klrdl.
GO; GO:0005529; F:sugar binding; IEA.
GO; GO:0007157; P:heterophilic cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 180; DB 11;
Pred. No. 9.2e-11;
25; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 AA.
                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00059; lectin c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PROSITE; PS00022; EGF_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
MEDLINE=22072192; PubMed=12077248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR006209; EGF like.
InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Natural killer cell receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.5%;
31.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pongo pygmaeus (Orangutan)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                            Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9600;
                                        OR CD94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POPY-CD94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OBMHY8;
                                        KLRD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
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KDSTCSHCPSCPILWTRNGS

7;

Length 179; Indels 84

--KDSTCSHCPSCPILWTRNGS

Q8MHY9; Q8MHY9;

SON DRANGE BY A REAL BY A

RESULT 7

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OBMHY9

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14 GTLGIICLSLITATLGILLKNSFTKLSIEPAFTPGPDIELQKDSDC--C-SCQEKWVGYRC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -- KDSTCSHCPSCPILWTRNGS 84
                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=22072192; PubMed=12077248;
Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;
Guethlein b.A., Flodin L.R., Adams E.J., Parham P.;
SNC ell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal
Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors
with MHC-C.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 HCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID----GW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THUMAN KIRPL, a novel member of the killer cell lectin-like receptor gene family: molecular characterization, genomic structure, physical mapping to the NK gene complex and expression analysis.";

EMEL, J. Immunol. 30:568-576(2000).

EMEL, AF15207; AAF37805.1; -.

GO; GO:001602; Camedrane; TAS.

GO; GO:0030106; F:MHC class I receptor activity; TAS.

Interpro; IPR001304; Lectin.C.

Pfam; PR00039; Lectin.C.

PROSITE; PS50041; C.LECT; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20135860; PubMed=10671213;
Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kucherlapati R.,
Fernandez-Ruiz E.;
Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 RWEGGPALS --- LRILINSLIQRCGAIHRNG-LQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 LWENGSSLSQYLFPLFETFNPKNCIAYNPNGNALDESCEDKNRYICKQQL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6; Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              674489E5EC6F8780 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 15, Last sequence update) Lectin-like receptor F1, splice variant 1 KLRF1-s1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.7%; Score 171.5; DB 6;
31.2%; Pred. No. 7.1e-10;
Live 16; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
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                                                                                                                                                                                                                                                                                                   44 GLLTVILMSLLMYQRILCCGS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00059; lectin c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PROSITE; PS00022; EGF_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 15, Created) (TrEMBLrel. 15, Last seq (TrEMBLrel. 24, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
   Chordata; (Primates; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 AA; 20536 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR006209; EGF like.
InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 31.2
nes 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
         Eukaryota; Metazoa;
                                  Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                  Mammalia; Euther
NCBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000
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SEQUENCE
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Matches
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                                                                                                                                  85 HCYYPSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID---GW 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----KDSTCSHCPSCPILWTRNGS 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 GTLGIICLSLTATLGILLKNSFTKLSIEPAFTPGPDIELQKDSDC--C-SCQEKWVGYRC 70
      MEDLINE=22072192; PubMed=12077248; Guethlein L.A., Flodin L.R., Adams E.J., Parham P.; Hubin L.A., Flodin L.R., Adams E.J., Parham P.; NK Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors with MHC-C.";
                                                                                            HCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID---GW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pongo pygmaeus (Orangutan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
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                                                                                                                                                                                                                                                          129 IWENGSSI.SQYLFPI.FETFNPKNCIAYNPNGNALDESCEDKNRYICKQQL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RWEGGPALS --- LRILTNSLIQRCGAIHRNG-LQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                  142 RWEGGPALS---LRILTNSLIQRCGAIHRNG-LQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 17.0%; Score 174.5; DB 6; Length 179; Local Similarity 31.8%; Pred. No. 3.4e-10; nes 54; Conservative 15; Mismatches 70; Indels 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 AA; 20520 MW; 674489E5FBD95CFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Natural viller cell receptor.
POPY-CD94.
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BMBL, AP470380, AAM78480.1; --
BMBL, AP470385, AAM78480.1; --
GO, GO:0004872, F:receptor activity; IEP
GO, GO:0005529; F:sugar binding; IEA.
InterPro: IPR006209; EGF like.
InterPro: IPR001304; Lectin_C.
Pfam; PF00059; lectin_C; l.
PROSITE; PS00041; C_TYPE_LECTIN_Z; l.
PROSITE; PS00042; EGF_L; l.
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                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Natural killer cell receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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Q8MJ14 Q8MJ14;

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RESULT 8 Q8MJI4

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Matches
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                                                                          44 GLLTVILMSLLMYQRILCCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFC 103
                                                                                                                                                      104 ADKGSHILITFPDNQGVKLFGEYLGQ-DFYWIGLRNID----GWRWEGGPALSLRIL----- 154
                                                                                                                                                                                 71 HCPSCPILWTRNGSHCYYFSMEKKDWNSSLKPCA-DKGSHLLTFPDNQGVKLFGEYLGQD 129
                                                                                                 130 FYWIGLRNIDG--WRWEGGPALSIRI-LINSLIQRCGAIHRNGLQASSCEVALQWICKK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yim D., Sotiriadis J., Kim K.-S., Shin S.-C., Jie H.-B.,
Rothschild M.F., Kim Y.B.;
"Molecular cloning, expression pattern, and chromosomal mapping of pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                      31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.4%; Score 169; DB 6; Length 15 30.3%; Pred. No. 1.1e-09; ive 22; Mismatches 55; Indels
                                   53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMEL; AF484234; AAL91547.1; -.
GO; GO:0005529; F:sugar binding; IEA.
InterPro; IPR001304; Lectin_C.
Pfam; PF00059; CLECT; 1.
SWART; SW00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SROUENCE 159 AA; 18056 MW; A19C3EEBABB32AA69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Type II membrane protein CD69 splice variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Type II transmembrane protein MDL-1 (C-type).
              Pred. No. 7.2e-10;
                                                                                                                                                                                                                                      155 -- TNSLIQRCGAIHRNGLQASSCEVALQWICK 184
                                                                                                                                                                                                                                                             159 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 AA.
                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Myeloid;
MEDLINE-99380598; Pubmed=10449773;
27.6%; Fir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36; Conservative
                                   42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel. 01-OCT-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40
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                Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD69."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
2028007
202000
AC 098000
AC 098000
DT 01-MA
DT 
                                   Matches
                                                                                                                                                                                                                                                                                                                                          RESULT 10
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63 SFSESPWKDSMDYCATQGSTLAIVNTPEKLKYLQDIAGIENYFIGLVRQPGEKKWRWINN 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 MVALGLLTVIL-----MSLLMYQRILCCGSKDS----TCSHCPSCPILWTRNGSHCYYF 89
                                                                                                                                                                                                                                                    The RANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).

BMBL; AR139769; AR702951: -
BMBL; AR139769; BAC29537.1; -
MGD; MGI:134515; Clecsfs.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016529; F:sugar binding; IEA.
InterPro; IPR001304; Lectin C.
Bakker A.B., Baker E., Sutherland G.R., Phillips J.H., Lanier L.L.; "Myeloid DAP12-associating lectin (MDL)-1 is a cell surface receptor involved in the activation of myeloid cells."; Proc. Natl. Acad. Sci. U.S.A. 96:9792-9796(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Agkisacutacin, a new fibrinolytic & anti-platelet protein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.3%; Score 168; DB 11; Length 165; 28.4%; Pred. No. 1.5e-09; Live 25; Mismatches 69; Indels 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agkistrodon acutus venom.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 PALSLRILINSLIQRCGAIHRNGL----QASSCEVALQWICK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 SVFNGNVTNODONFDCVTI---GLTKTYDAASCEVSYRWICE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 AA; 19055 MW; 626D64392A513282 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 AA
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PRINTS; PR01504; PRCEATITSAP.
SMART; SM00034; CIECT; 1.
PROSITE; PS00615; C TYPE_LECTIN 1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50041; C TYPE LECTIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P23807; IIXX.
GO; GO:0005529; F:sugar binding; IEA.
InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2000 (TEMBLE). 15, Created)
01-0CT-2000 (TEMBLE). 15, Last seq
01-0CT-2003 (TEMBLE). 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE=Bone;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF176421; AAF26287.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agkisacutacin B chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00034; CLECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
tes 46; Conserv
                                                                                                                                      [2]
SEQUENCE FROM N.A.
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100 WIGLNFTLSGKSWKWINGSFLNSNILPIFGDAKEDCCVYISKTQCISDYCAAKNRWICQK 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 WIGLR-NIDG--WRWEGGPALSLRILT---NSLIQRCGAIHRNGLQASSCEVALQWICKK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 TCPMHWKRIRDKCLYFSETSKPWNDSLADCSTRESSLLLIQDQEELRLMQNLINKEGILF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21308528; PubMed=11414735;
Yim D., Jie H.B., Sotiriadis J., Kim Y.S., Kim Y.B.;
"Molecular cloning and expression pattern of porcine myeloid DAP12-
                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                      Govaerts M.M., Goddeeris B.M.; "Homologues of natural killer cell receptors NKG2-D and NKR-P1
Natural killer cell receptor protein 1 variant 1 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 AA; 18653 MW; 40C29ABE136E76D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24F9AA44A19EAFB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                associating lectin-1.";

Cell. Immunol. 209:42-48(2001).

EMBL; AF28549; ABC29427.1; -.

GO; GO:0005529; F:sugar binding; IEA.

GO; GO:0007157; P:heterophilic cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.8%; Score 163; DB 6;
31.1%; Pred. No. 4.9e-09;
iive 20; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myeloid DAP12-associating lectin short form.
                                                                                                                                                                                                                                                             Immunopathol. 80:339-344 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 AA
                                                                                                                                                                                                                                                             Vet. Immunol. Immunopathol. 80:339-344(20 MBL; AR232886; ARX73811.1; -- GO, GO:0004872; F:receptor activity; IEA. GO, GO:0005529; F:sugar binding; IEA. InterPro; IRROlast, Lectin_C. InterPro; IRROlast, Lectin_C. SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001304; Lectin_C.
Pfam; PF00059; Lectin_c; 1.
SWART; SN00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                          PROSITE, PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                     TISSUE=Spleen;
MEDLINE=21351526; PubMed=11457486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18648 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 31.14
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  161
                                                                                                                                                                                                                                             expressed in cattle.";
                                                                                           Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 AA;
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                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                             NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                   161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161
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NON TER
NON TER
SEQUENCE
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Q9GLF4
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                                                                                                                                                                                         DWNSSLKFCAD--KGSHLLTFPDNQG----VKLFGEYLGQDFYWIGLRNI-DG--WRWEG 145
                                                                                                                                                                                                                            45 TWADAEKFCTQQHKGSHLASFHSSEEADFVVTLTTPSLKTDLVWIGLKNIWNGCYWKWSD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 TWADAEKFCTQQHKGSHLASFHSSEEADFVVTLTTPSLKTDLVWIGLKNIWNGCYWKWSD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94
                                                                                                                 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 LSRFAMVALGLLTVILMSLLMYQRILCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKK
                                                                                                             35 LSRFAMVALGLLTVILMSLLMYQRILCCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKK
                                                                                                                                                  MGRFIFVSFGLLVVFL-----SLSGTAADCPSD---WSSYEGHCYKPFDEPK
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Deinagkistrodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25;
                                                                            25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.9%; Score 163.5; DB 13; Length 146; 30.2%; Pred. No. 3.9e-09;
                                       DB 13; Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71; Indels
                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yu H., Xiang K., Wang Y., Liu J.;
"B chain of agkisacutacin from Deinagkistrodon acutus.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AYO91756, AAM22785.1;
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PIR, JC7135, JC7135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; JC7135; JC7135.

QC; GO:005529; F:sugar binding; IEA.

InterPro; IPR001304; Lectin C.

InterPro; IPR003990; Pancreatis ac.

Ffam; PR00059; lectin C; 1.

PRINTS; PR01504; PRCEEDITSAP.

SMART; SM00034; CLECT; 1.

PROSITE; PS00615; C TYPE LECTIN 1; 1.

PROSITE; PS50041; C TYPE LECTIN 2; 1.
 7360B6D6864131BB CRC64;
                                                                                                                                                                                                                                                               GPALSLRILINSLIQRCGAIHRNGLQASSCEVALQWICK 184
                                                                                                                                                                                                                                                                                                  GTKLDYKDWREQFECLVSRTVNNEWLSMDCGTTCSFVCK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPALSLRILINSLIQRCGAIHRNGLQASSCEVALQWICK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 GTKLDYKDWREQFECLVSRTVNNEWLSMDCGTTCSFVCK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                     15.9%; Score 163.5; DB 13; 30.2%; Pred. No. 3.9e-09; tive 15; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 AA
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8; Gaps

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Length 161;

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7;
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Best Local Similarity 29.1%; Pred. No. 8.1e-09;
Matches 48; Conservative 25; Mismatches 66; Indels 26; Gaps
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SMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLKNIDGWRWE 144 :	
88 YFSMEI : 61 FLSTSI	

ŏ qq Search completed: August 10, 2004, 16:44:03 Job time : 33 secs

QY Db

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

- protein search, using sw model OM protein Run on:

August 10, 2004, 16:35:35; Search time 47.5 Seconds (without alignments) 1118.293 Million cell updates/sec

US-09-811-367B-3

1 MADSSIYSTLELPEAPQVQD.....GLQASSCEVALQWICKKVLY 188 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1586107 seqs, 282547505 residues Searched:

1082526 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 188

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A_Geneseq_29Jan04:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. geneseqp2004s:*

STIMMARTES Re

	Description	Aae11760 Mouse mas	3 Mammalia		Rat	Part		Human	CD94.	Human	6 Human	Human	Human	. ,	Human		Human	Human	Human	Secret		Human	Human	Human	Human	Human
SUMMAKIES	ID	AAE11760	AAR77033	AAW88277	AAE11761	AAR77472	AAW88267	AAW64791	AAW40222	ADE76965	AAM80296	ABG72616	AAM80302	AAW27288	ADC38664	AAU19660	ABP47880	ADC10842	AAU00673	ABO32541	AAU19816	ABP48036	ADC10998	AAU19836	AAU19690	ABB15422
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ò	Query Match	100.0	81.4	81.4	81.4	ص	21.6	7			•	16.3	16.3			5	15.2	5	5.	15.0	14.4	14.4	14.4	14.4	14.4	14.4
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	esult No.	1	7	m	4	w	9	7	œ	σ	10	11	12	13	14	72	16	17	18	19	20	21	22	23	24	25

Human Human Human	Adc10872 Human ext Adc11018 Human pro Aaw36957 Protein e		Aam26602 Peptide # Abb27967 Human pep		Aameeszs Human Don Aam53935 Human bra	Abg47989 Human liv	Human	Aau00675 Human INT Abo32547 Secreted	Aam25760 Human pro	Aam51544 Snake ven
ABB17909 ABP48056 ABP47910	ADC10872 ADC11018 AAW36957	AAM14192 ABB33139	AAM26602 ABB27967	ABB18604	AAM53935	ABG47989 AAM01928	ABG35971	ABO32547	AAM25760	AAM51544
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ALIGNMENTS

Mouse mast cell function associated antigen (MAFA) protein. AAE11760 standard; protein; 188 AA. (first entry) 18-DEC-2001 AAE11760; HANDER STANDER
Mouse; pharmaceutical composition, mast cell function associated antigen, MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL; immunosuppressive; cytostatic

Mus sp

64. .188 /note= "Extracellular domain" Location/Qualifiers 64. .188 WO200170805-A2 Domain

27-SEP-2001

16-MAR-2001; 2001WO-US008596 L7-MAR-2000; 2000US-0190716P

(GEMI-) GEMINI SCI INC.

Ë Takahashi N, Mikayama

2001-611482/70. WPI; 2001-611482/ N-PSDB; AAD18735.

Pharmaceutical composition for treating tumor by stimulating cytotoxic activity of natural killer cell or T-cell, comprises an agent that binds to mast cell function-associated antigen ligand on target cell.

Example 1; Page 19; 49pp; English.

The present invention relates to a pharmaceutical composition comprising an agent which specifically binds to a mast cell function associated antigen (WAFA) ligand on a target cell, and prevents or inhibits natural killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA ligand and a pharmaceutically acceptable excipient. The invention is useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA binding to a ligand on a target cell, by contacting the pharmaceutical

combination with the MAFA to prevent inflammatory and allergic reactions

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composition in vitro, ex vivo or in vivo by administering the composition an amount sufficient to inhibit cell surface MAFA binding to the ligand on the target cell. The agent or the composition is useful for treating a tummour by stimulating the cytotoxic activity of an NK cell or treating tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic tumour cell. The invention is also useful for inhibiting an activity of NK cell or a receiptible tumour cell. The invention is also useful for inhibiting an activity of NK cell or a T-cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mast cell function-associated antigen; MAFA; soluble; ligand; identification; screening; inflammation; inflammatory; allergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel DNA encoding a mast cell function-associated antigen (MAFA) - useful for screening for ligands of MAFA which are useful for prevention of inflammatory and allergic reactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A soluble form of mast cell function-associated antigen (MAFA) can be produced by recombinant techniques for use in the ligand- screening assay. The ligands that are identified may be used alone or in
                                                                                                                                                                                                                                                        1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLITVILMSVLLMYQRIL
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                                                                                                                                                                      100.0%; Score 1029; DB 4; 100.0%; Pred. No. 6.6e-103;
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(RYCU/) RYCUS
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                                                                                                                                                   CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120
                                                                                                                                                                   This is the amino acid sequence of rat mast cell function-associated antigen (MAFA), a type II membrane glycoprotein found on mast cells and basophils. The invention relates to cloning of the human MAFA molecule (see AAW82265) and to the discovery of splice variants (see AAW882667) of human MAFA that are not found in rat. Polypeptides and synthetic
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                                                                                                               1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL
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                                                                        21; Indels
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                                             81.4%; Score 838; DB 2;
80.7%; Pred. No. 3.2e-82;
ive 15; Mismatches 21.
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'note= "Asn is N-glycosylated"
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                                                                                                                                                                                                                                                                                                                                                     AAW88277 standard; protein; 188 AA
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                                                                         151; Conservative
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N-PSDB; AAV84222.
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                                                             Similarity
                     Sequence 188 AA;
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                                                                                                                                                                                               MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL 60
peptides (see AAW88258-64) based on human MAFA and human truncated MAFA, and polynucleotides encoding them, can be used in methods for the treatment of inflammatory and allergic diseases (e.g. rheumatoid arthritis and asthma), and tumour growth
                                                                                                                                            Gaps
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                                                                                                              Length 188;
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15; Mismatches 21
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Rat mast cell function associated antigen (MAFA) protein. AAE11761 standard; protein; 188 (first entry) 18-DEC-2001 AAE11761; AAE1176. RESULT HID STANDARD
Ā.

mast cell function associated antigen; Rat; pharmaceutical composition; mast cell function associated antigen MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CIL; immunosuppressive; cytostatic

Rattus norvegicus.

WO200170805-A2

27-SEP-2001

16-MAR-2001; 2001WO-US008596.

17-MAR-2000; 2000US-0190716P

(GEMI-) GEMINI

Mikayama Takahashi N,

2001-611482/70. N-PSDB; AAD18736 irmaceutical composition for treating tumor by stimulating cytotoxic sivity of natural killer cell or T-cell, comprises an agent that binds mast cell function-associated antigen ligand on target cell. Pharmaceutical activity of

Example 1; Page 19; 49pp; English.

The present invention relates to a pharmaceutical composition comprising an agent which specifically binds to a mast cell function associated antigen (WAFA) ligand on a target cell, and prevents or inhibits natural killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA ligand and a pharmaceutically acceptable excipient. The invention is useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA binding to a ligand on a target cell, by contacting the pharmaceutical composition in vitro, ex vivo or in vivo by administering the composition

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0
to the subject, to NK or T-cell or the target cell e.g. tumour cell, in an amount sufficient to inhibit cell surface MAPA binding to the ligand on the target cell. The agent or the composition is useful for treating a tumour by stimulating the cytotoxic activity of an NK cell for a cytotoxic tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic tumour cell. The invention is also useful for inhibiting an activity of NK cell or a T-cell. The present sequence is rat MAPA protein
                                                                                                                                                                                                                                                                                                                                                        CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120
                                                                                                                                                                                                                                                                                                        CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120
                                                                                                                                                                                                                                                                                                                                        LFGEYLGQDFYWIGLRNIDGWRWEGGPALSLRILTNSLIQRCGAIHRNGLQASSCEVALQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mast cell function-associated antigen; MAFA; soluble; ligand; identification; screening; inflammation; inflammatory; allergy; allergic;
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                                                                                                                                                                                                                                             MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL 60
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useful for prevention
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                                                                                                                                                        Length 188;
                                                                                                                                                                                                                 1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTV
                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel DNA encoding a mast cell function-associated useful for screening for ligands of MAFA which are
                                                                                                                                                                                    21;
                                                                                                                                                      Score 838; DB 4;
Pred. No. 3.2e-82;
15; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of inflammatory and allergic reactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; 114 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 38; 54pp; English.
                                                                                                                                                      81.4%;
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                                                                                                                                                                                 Matches 151; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                  WICKKUL 187
                                                                                                                                                                                                                                                                                                                                                                                                                               WICEKVL 187
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                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR77472 standard;
                                                                                                                          Sequence 188 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09527734-A1.
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                                                                                                                                                     Query Match
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85 HCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID---GW 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a novel human natural killer (MK) cell surface antigen, Kp43. This sequence can be used in a method resulting in the production of recombinant protein expressed by NK and T cells, which may inhibit cell-mediated cytotoxicity, e.g. in transplant rejection or autoimmune diseases, or may be used to produce antibodies for diagnostic or therapeutic use
                                                                                                                                                                                                                                                                                                                                       Kp43; human; natural killer cell surface antigen; NK; T cell; inhibitor; cell-mediated cytotoxicity; transplant rejection; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding natural killer cell surface antigen Kp43 - and transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -KDSTCSHCPSCPILWTRNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 GTLGIİCLSLMATLGILLKNSFTKLSIEPAFTPGPNIELQKDSDC--C-SCQEKWYGYRC
                                                                             ----ISSNSFVQTCGALTKNGLQASSCEVPLH
    CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK
                                                            121 LFGEYLGQDFYWIGLRNIDGWRWEGGPALSLRILINSLIQRCGAIHRNGLQASSCEVALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phillips JH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 179;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beltran JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.3%; Score 178.5; DB 2; llarity 31.8%; Pred. No. 7.5e-11; Conservative 17; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cells for producing recombinant Kp43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lopez-Botet M,
                                                                                                                                                                                                                           AAW64791 standard; protein; 179 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Col 31-32; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 GLLTVILMSLLMYQRILCCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93US-00175339.
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(LOPE/) LOPEZ-BOTET M.
(BELT/) BELTRAN J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lanier LL, Chang C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-530877/45.
                                                                                                                                                                                                                                                                                 (first
                                                                                                                        181 WICKKV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 54; Conserv
                                                                                                                                                                                                                                                                                                              Human Kp43 protein
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                                                                                                                                                     92 WVCKKV
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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Matches
                                                                                                                                                                                               RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptide having a sequence corresponding to human mast cell function—associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic diseases, and tumour growth.
                                                                                              134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is the amino acid sequence of human mast cell function- associated antigen (MAFA) splice variant huMAFA(ES/4-), which lacks the C-lectin-like domain of human MAPA (see AAMB8265) but retains the intracellular and transmembrane domains as well as the extracellular C-terminal tail. Truncated MAFA polypeptides including huMAFA(E3/4-), and polynucleotides encoding them, as well as synthetic peptides (see AAWB8258-64, AAWB8268-72), can be used be used in compositions for the treatment of inflammatory and allergic diseases (e.g. rheumatoid arthritis and asthma), or tumour growth
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                                                                                              CPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIG
                                                                                                                        1 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                  Gaps
                                                                                                                                                      LRNIDGWRWEGGPALSLRILTNSLIQRCGAIHRNGLQASSCEVALQWICKKVL 187
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0
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                                      Length 114;
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                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Williams DH;
                                    Score 551; DB 2; L
Pred. No. 1.9e-51;
9; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 222.5; DB 2;
Pred. No. 5.9e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Mismatches
                                                                                                                                                                                                                                                                                                                                                Human MAFA splice variant huMAFA(E3/4-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lamont A,
                                                                                                                                                                                                                                                            Ä
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                                                                                                                                                                                                                                                          standard; protein; 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.6%;
30.1%;
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                                       53.5%;
84.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-059806/05.
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                                                     Local Similarity
les 95; Conser
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            Sequence 114 AA;
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                                                                                                                                                                                                                                                                                                                   29-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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Best Local S
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                                       Query Match
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Matches
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70 84

Human protein expressed in a liver disorder #36.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human macrophage antigen - used for decreasing apoptosis associated with osteoarthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTLGIICLSLMATLGILLKNSFTKLSIEPAFTPGPNIELQKDSDC--C-SCQEKWVGYRC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KDSTCSHCPSCPILWTRNGS 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID---GW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
129 LWENGSALSQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQQL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RWEGGPALSLRILTN---SLIQRCGAIHRNG-LQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                     TMAH; apoptosis; osteoarthritis; diagnosis; treatment.
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                                                                               AAW40222 standard; peptide; 179 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 47; 58pp; English.
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                                                                                                                                     entry)
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                                                                                                                                                                                                                                                                                                                                                (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                           Au-Young J,
                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-130617/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 179 AA;
                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                           22-JUL-1997;
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                                                                                                                                 07-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                        Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JAN-2004
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                                                                                                        AAW40222
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ID ADE7
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AC ADE7
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DT 29-5
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                                                                   AAW40222
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The invention relates to a composition comprising several CDNAs that are differentially expressed in a liver disorder. The composition is useful for treating liver disorder such as hyperlipidaemia, hypertension, type II diabetes, tumours of the liver and disorders of the inflammatory and immune response. The composition is useful for a high-throughput method of screening several molecules or compounds to identify a ligand which specifically binds a CDNA. A protein encoded by the CDNA is useful for a high-throughput method for using a protein to screen several molecules or compounds to identify at least one ligand which specifically binds the compounds to identify at least one ligand which specifically binds the protein which involves compounds under conditions to allow specific compounds and detecting specific binding between the protein and a condition of binding, and detecting specific binding between the protein and and composition is useful for detecting and composition is useful for detecting and to design a treatment regimen and to monitor the efficacy of treatment. The present sequence represents the amino acid a protein encoded by a CDNA differentially expressed in a protein and an expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                          Composition comprising several cDNAs that are differentially expressed in treated human C3A liver cell cultures, useful for treating liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70
                              human; liver disorder; hyperlipidaemia; hypertension; type II diabetes; tumour; liver; inflammatory disorder; immune response disorder; high-throughput screening; differential gene expression; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *KDSTCSHCPSCPILWTRNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 HCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID---GW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.3%; Score 178.5; DB 8;
31.8%; Pred. No. 7.5e-11;
ive 17; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 130; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM80296 standard; protein; 142 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 GLLTVILMSLLMYQRILCCGS
                                                                                                                                                                                                                 30-JUL-2001; 2001US-00919039.
                                                                                                                                                                                                                                                        28-JUL-2000; 2000US-0222113P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 31.0%
For 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-031227/03.
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                                                                                                                                             US2003108871-A1
                                                                                                                                                                                                                                                                                            (KASE/) KASER
                                                                                                                                                                                                                                                                                                                                                                                                                    Composition
                                                                                                                                                                                 12-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders
                                                                                                                                                                                                                                                                                                                                Kaser MR;
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                                                                                                          Ношо
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AAM80296
ID AAM8
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AC AAM8
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ABG72616 standard; protein; 142 AA.

RESULT 11 ABG72616 (first entry)

12-FEB-2003

ABG72616;

cell proliferation; cell differentiation; gene therapy;

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Nucleic acids encoding polypeptides with cytokine-like activities, useful
                                                    vaccine; peptide therapy; stem cell growth factor; haematopolesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 6210-6211; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                             in diagnosis and gene therapy.
                                                                                                                                                                                                   01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-0065561.
20-OCT-2000; 2000US-00653325.
30-NOV-2000; 2000US-00728422.
                                                                                                                                                               03-FEB-2000; 2000US-00496914.
27-APR-2000; 2000US-00560875.
20-UUX-2000; 2000US-00590075.
19-UUL-2000; 2000US-00620325.
                          Human protein SEQ ID NO 3948.
                                                                                                                                               05-FEB-2001; 2001WO-US004098.
        06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                       WPI; 2001-476283/51.
                                                                                                                                                                                                                                                                          zhao QA, W
                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                    Liu C,
                                                                                                                                                                                                                                                                                                                  N-PSDB; AAK53429.
                                           cytokine;
                                                                                                           WO200157190-A2.
                                                                                          Homo sapiens.
                                                                                                                             09-AUG-2001
                                                                                                                                                                                                                                                                   Tang YT,
Ma Y, Zh
Xue AJ,
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Xu C, Cao Y; . Chen R, Wang ZW;

Drmanac RT, Asundi V, Zhou P, X: Wang D, Wang J, Zhang J, Ren F, Wejhrman T, Goodrich R;

Asundi V,

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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to eytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynuclaotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, or activity, immunomodulatory activity and activity, and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Noter Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 SHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQCVKLFGEYLGQD 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 FYWIGL-RNIDGWRWEGGPALSLRIL----TNSLIQRCGAIHRNGLQASSCEVALQWICK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 ARCQQCPPGWVLSBEHCYYFSAEAQAWEASQAFCSAYHATLDFLLSHTQ--DFLGRYPVSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.3%; Score 167.5; DB 4; Length 142; 30.6%; Pred. No. 8.6e-10; ive 15; Mismatches 62; Indels 7.
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nes 37; Conservative
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Matches
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K 139

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The invention relates to an isolated polynucleotide encoding a cytokine or cell proliferation/differentiation-related protein (or the mature protein or active domain), sequences greater than 0% identical to it or sequences complementary to it. Also included are the encoded proteins, expression vectors, transformed host cells, antibodies, and identifying a compound that binds to the polypeptide. The polynucleotide, polypeptides encoded by it, or antibodies to the polypeptides are useful in therapeutic, diagnostic or research methods. They are particularly useful for diagnosing, treating or preventing e.g. anaemias, wounds, ulcers, thrombocytopaenia, osteoporosis, osteoarthritis, inflammations. Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral scleonis, stroke, immune deficiences (e.g. human amyotrophic lateral scleonis, stroke, immune deficiences (e.g. human
                                                                                                                                                 wound; ulcer; thrombocytopaenia; osteoporosis; osteoarthritis; inflammation; Alzheimer's disease; Parkinson's disease; stroke; Huntington's disease; amyotrophic lateral sclerosis; HIV; munue deficiency; human immunodeficiency virus infection; evere combined immunodeficiency; infection; autoimmune disorder; rheumatoid arthritis; Guillain-Barre syndrome; graft-versus-host disease; cancer; thyroid cancer; lung cancer; syndrome; graft-versus-host disease; kaposi's sarcoma; brain tumour; prostate cancer; ovarian cancer; leukaemia; inflammatory disorder; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunodeficiency virus (HIV), severe combined immunodeficiency or infections), autoimmune disorders (e.g. rheumatoid arthritis, Guillain-Barre syndrome or graft-versus-host disease), cancers (e.g. thyroid cancer, lung cancers, small cell carcinoma, Kaposi's sarcoma, brain tumours, prostate cancer, ovarian cancer or leukaemias), or inflammatory disorders (e.g. inflammatory bowel disease or Crohn's disease). The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yang Y;
                                                                                                                                Human; cytokine; cell proliferation; cell differentiation; anaemia;
                                                                                             Human cytokine or cell proliferation/differentiation protein #6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wounds, ulcers, thrombocytopenia, osteoporosis, inflammations
Alzheimer's disease, stroke, autoimmune disorders or cancers.
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                                                                                                                                                                                                                                                                                                                                 Crohn's disease; food supplement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goodrich R,
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27-APR-2000; 2000US-00560875.
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DRMANAC R T.
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GOODRICH R.
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ASUNDI V.
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(DRMA/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSWVGAWRGPQGWHWIDEAPLPPQLLPEDGEDNLDINCGALEEGTLVAANCSTPRPWVCA 138
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                                                                                                                                                                                                                                                                                                                                                                                  Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
polynucleotides and proteins are useful for screening peptides or small molecule inhibitors or agonists that are useful for treating these diseases. The polypeptide is also useful as molecular markers, or as a food supplement. The present sequence is a cytokine or cell proliferation/differentiation-related protein of the invention
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R, Wang ZW;
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J, Zhang J, Ren F, Chen
Goodrich R;
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                                                                                                                                                                                                                                                                                       62;
                                                                                                                                                                                                                          16.3%; Score 167.5; DB 6
30.6%; Pred. No. 8.6e-10;
ive 15; Mismatches 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM80302 standard; protein; 160 AA.
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Wang D, Wang J
Wejhrman T, G
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27-APR-2000; 2000US-00560875.
20-JUN-2000; 2000US-00598075.
19-JUL-2000; 2000US-00620325.
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2000US-00693325.
2000US-00728422.
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les 37; Conservative
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Ma Y, Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-476283/
N-PSDB; AAK53435.
                                                                                                                                                                         Sequence 142 AA;
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         production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
(AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                           70 SHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQD 129
                                                                                                                                                                                                                                                                                                               130 FYWIGL-RNIDGWRWEGGPALSIRIL----TNSLIQRCGAIHRNGLQASSCEVALQWICK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ed protein; anti-inflammatory; immune stimulant; suppressant; cytokine; autoimmune disease; regulator; activin; inhibin; G52-24.
 or which may induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding novel secreted proteins - useful e.g. as an anti-inflammatory, immune stimulant or suppressor, etc.
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                  7;
                                                                                                                                                                                          Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "predicted mature amino acid sequence"
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                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Merberg
cell proliferation or cell differentiation
                                                                                                                                                                                                                   62;
                                                                                                                                                                                        DB 4;
                                                                                                                                                                                       16.3%; Score 167.5; DB 30.6%; Pred. No. 1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Racie LA, Lavallie ER,
                                                                                                                                                                                                                15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW27288 standard; protein; 181 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .40
/label= signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41. .181
/label= G52-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human G52-24 secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-00635311
97US-00781226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-US006125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mccoy JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-535835/49.
                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAT91295.
                                                                                                                                                              Sequence 160 AA;
                                                                                                                                                                                                                                                                                                                                                    K 185
                                                                                                                                                                                                                                                                                                                                                                             K 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9740151-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-0CT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spaulding
                                                                                                                                                                                                                                                                                                                                                    185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
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                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
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25-0CT-1996
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                                                        10-APR-1997
                                                                       02-JUN-1997
                                                                                  05-SEP-1997
                                                                                                                                                        Merberg D,
Kelleher K;
                                                                                                                                              Jacobs K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU19660;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; allergic reaction; asthma; myeloid cell deficiency; lymphoid cell deficiency; osteoporosis; osteoarthritis; peripheral nervous system disease; peripheral neuropathy; Alzheimer's disease; Parkinson's disease; coagulation disorder; inflammatory disease; systemic inflammatory response syndrome; SIRS; ischaemia-reperfusion injury; Crohn's disease; anaphylaxis; hypersensitivity; regeneration; neural cell proliferation; fertility; tumour; chemokine; human; secreted protein.
                                 a clone, G52-24 (ATCC 98028), derived from a human PBMC cDNA library. The mucleic acid and encoded G52-24 secreted protein can be used for research purposes (as markers for tissues, molecular weight markers for gels, primers, probes, etc.), for nutrition (as C, N or carbohydrate source), as a cytokine for cell proliferation and differentiation activity, as immune stimulants or suppressors e.g. for viral, bacterial or fungal infections, for autoimmune diseases such as multiple sclerosis or
                                                                                                                                                                                                                                                                                                            -----PA 148
                                                                                                                                                                                                                                                                                                                                  SSORFCDSODADLAQVESFOELNFLLRYKGPSDHWIGLSREQGOPWKWINGTEWTROFFI 147
                                                                                                                                                                                                                                                            97
                                                                                                                                                                                                                                                                                  LFFLIMFLTIIVCGMVAALSAIRANCHQEPSVCLQAACPESWIGFQRKCFYFSDDTKNWT 87
                        isolated from
                                                                                                                       systemic lupus erythematosus, to regulate haematopoiesis, for tissue growth, as an activin or inhibin, or having chemotactic, chemokinetic, haemostatic and thrombolytic, receptor/ligand, anti-inflammatory or
                                                                                                                                                                                                                                                           LMSLLMYQRILCCG-----SKDSTCSHCPS-----CPILWTRNGSHCYYFSMEKKDWN
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                  29;
                                                                                                                                                                                                            Length 181;
                                                                                                                                                                                                                                                                                                             SSIKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNIDG--WRWEGG-
                       This sequence represents a novel secreted protein, G52-24,
                                                                                                                                                                                                                                   67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immune disorder; severe combined immunodeficiency; SCID;
                                                                                                                                                                                                                                                                                                                                                                                   ----AGECAYLNDKGASSARHYTERKWICSK 176
                                                                                                                                                                                                                                                                                                                                                             LSLRILINSLIQRCGAIHRNGLQASSCEVALQWICKK 185
                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                           Score 160.5; DB 2. Pred. No. 6.8e-09;
                                                                                                                                                                                                                                   19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC38664 standard; protein; 181 AA
Claim 8; Page 59; 81pp; English.
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96US-00635311.
96US-00659224.
96US-00664596.
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96US-00686878.
96US-00701819.
96US-00721488.
96US-00721798.
                                                                                                                                                                                                            15.6%;
26.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-00514014
                                                                                                                                                            tumour inhibitory activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein #11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                   42; Conservative
                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                     Sequence 181 AA;
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                                                                                                                                                                                                                                                                                                                                                                                     148 LG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-AUG-1996;
27-SEP-1996;
27-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-1996;
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                                                                                                                                                                                                             Query Match
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The invention relates to a protein comprising fully defined AZ302 I

C protein or BD127 1 6 protein. The polynucleotides are useful for

C expressing recombinant proteins for analysis and are also useful as

C chromosome markers or tags to identify chromosomes or to map related gene

C chromosome markers or tags to identify chromosomes or to map related gene

CC constituent introgen source and carbohydrate source. The proteins are useful

CC source, nitrogen source and carbohydrate source. The proteins are useful

CC combined immunodeficiency (SCID), autoimmune disorders (e.g. multiple

CC combined immunodeficiency (SCID), autoimmune disorders (e.g. multiple

CC reactions (e.g. asthma), myeloid or lymphoid cell deficiencies,

CC reactions (e.g. asthma), myeloid or lymphoid cell deficiencies,

CC reactions (e.g. asthma), myeloid or lymphoid cell deficiencies,

CC osteoporosis or osteobarthritis, peripheral nervous system disease),

CC peripheral neuropathy, Alzheimer's disease, Parkinson's disease),

CC coagulation disorders, inflammatory diseases, Parkinson's disease),

CC capulation myproxensitivity. Proteins are also useful for inducing

CC tumour immunity, for inducing bone, cartilage, tendon, ligament and/or

CC nerve growth or regeneration, for proliferating neural cells and for

CC inhibiting tumour growth. Proteins are also useful as othendrine for

CC inhibiting tumour growth. Proteins are also useful as othendrine for

CC inhibiting tumour growth. Proteins are also useful as othendrine for

CC inhibiting tumour growth. Proteins are also useful as othendrine for

CC inhibiting tumour growth. Proteins are also useful as offence represents

CC sequence represents the amino acid sequence of a human secreted protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---CPILWTRNGSHCYYFSMEKKDWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 LFFLIMFLTIIVCGMVAALSAIRANCHQEPSVCLQAACPESWIGFQRKCFYFSDDTKNWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteins A23021 encoded by clone A23021 from human adult colon, and BD12716 encoded by clone BD12716 from human fetal kidney cDNA library, useful for treating e.g. multiple sclerosis and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                Collins-Racie LA, Evans C;
Spaulding V, Carlin-Duckett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 SSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNIDG--WRWEGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LG-----AGECAYLNDKGASSARHYTERKWICSK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67;
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26.8%; Pred. No. 6.8e-09;
live 19; Mismatches 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bowman MR,
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96US-00721926.
96US-00738367.
96US-00739775.
97US-00783395.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treacy M,
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N-PSDB; ADC38663.
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nes 42; Conserv
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2000US-0232398P.
2000US-0232399P.
2000US-0232400P.
2000US-0232401P.
2000US-0233064P.
2000US-0233064P.
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2000US-0249966P.
2000US-0249937P.
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  2000US-0232081P.
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2000US-0232397P.
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2000US-0234997P.
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2000US-0246526P
2000US-0246526P
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    Human; secreted extracellular matrix protein; immunomodulatory; Anti-HIV; antianemic; antirheumatic; antisclerotic; cardiant; vascular; ereebroprotective; thrombolytic; antimicrobial; ophthalmic; cytostatic; antialzheimers; immune/autoimmune disease; HIV infection; anaemia; human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis; cancers; hyperproliferative disorder; breast neoplasm; melanoma; Sezary syndrome; Gaucher's disease; neurological diseases; Alzheimer's disease; Parkinson's disease; cardiovascular disorder; cardiac arrest; tachycardia; angina; infection; corneal infections; wound healing; immunogen; gene therapy; antisense; food additive.
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                                                                                                                                                                                                                                                                                                                     2000US-0179065P.
2000US-018664P.
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2000US-0189124P.
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04-DEC-2001
                           Human novel
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The invention relates to isolated nucleic acid molecules encoding novel human secreted extracellular matrix proteins (SPS). The polymucleotides and proteins are used to prevent, treat a medical condition in e.g. thumans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased expression of SPs. The SP polymucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisense molecules may be administered to treat diseases by gene therapy. Antisense molecules may be administered to down regulate expression of SPs by binding with the cells own genes and probes in diagnostic assays. The SPs may also be used as DNA probes in diagnostic assays. The SPs may also be used as antigens to probuce antibodies and to identify modulators (agonists and antagonists) of the SPs. The anti-(SP) antibodies and antagonists and antagonists of the SPs. The anti-(SP) antibodies and antagonists and antagonists of down regulate expression and activity of SP and as disorders include for example: immune/autorimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease), neurological diseases (e.g. Alzheimer's disease, Parkinson's disease), neurological diseases (e.g. corneal infections). Other uses include wound healing, maintenance (e.g. corneal infections). Other uses include wound healing, maintenance of primary corners before transplantation, support of cell culture of primary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid molecules encoding human secreted extracellular matrix proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers.
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2000US-0251868P.
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N-PSDB; AAS31231.
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Search completed: August 10, 2004, 16:42:20

Job time : 48.5 secs

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GenCore version 5.1.6
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- protein search, using sw model OM protein

August 10, 2004, 16:44:06; Search time 39.5 Seconds (without alignments) 1492.972 Million cell updates/sec Run on:

US-09-811-367B-3 1029 1 MADSSIYSTLELFEAPQVQD.......GLQASSCEVALQWICKKVLY 188 Title: Perfect score:

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1291235 seqs, 313682936 residues Searched:

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Minimum DB seq length: 0 Maximum DB seq length: 188

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Listing first 45 summaries

Database

Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Flack & echology	Semience 5, Appli	Sequence 130. App	Sequence 10. Appl	Sequence 22, Appl	Sequence 310. App	Seguence 310. App	Sequence 98. Appl	Sequence 98. Appl	Sequence 4. Appli	Seguence 466. App	Segmence 466. App	Segmence 340. App	Segmence 486, App	Sequence 340, App
SOFTERING	ID	US-09-811-367R-3	US-09-811-367B-5	US-09-919-039-130	US-10-335-009-10	US-10-114-893-22	US-09-764-870-310	US-10-125-540-310	US-09-759-130B-98	US-10-741-790-98	US-10-335-009-4	US-09-764-870-466	US-10-125-540-466	US-09-764-870-340	US-09-764-870-486	US-10-125-540-340
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o¥.	Query Match	100.0	81.4	17.3	17.3	15.6	15.2	15.2	15.0	15.0	14.7	14.4	14.4	14.4	14.4	14.4
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61 CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120

Sequence 486, App Sequence 33902, A Sequence 108, App Sequence 108, App	Sequence 1275, Ap Sequence 5855, Ap Sequence 11, Appl Sequence 32, Appl	Sequence 1, Appli Sequence 83, Appl Sequence 83, Appl Sequence 6, Appli	0 0 0 0 0	Sequence 85, Appl Sequence 85, Appl Sequence 86, Appl Sequence 86, Appl Sequence 12, Appl	Sequence 3, Appli Sequence 90, Appli Sequence 67, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 6, Appli
14 US-10-125-540-486 9 US-09-864-761-33902 10 US-09-759-130B-108 16 US-10-741-790-108	12 US-10-296-115-1275 14 US-10-106-698-5855 10 US-09-284-320-11 13 US-10-114-893-32 14 US-10-088-859-2	14 US-10-179-528-1 10 US-09-759-130B-83 16 US-10-741-790-83 9 US-09-944-807-6	10 US-09-766-511B-55 14 US-10-270-470-2 10 US-09-759-130B-100 16 US-10-741-790-100	16 US-10-741-790-85 10 US-10-741-790-85 10 US-09-759-130B-86 16 US-10-741-790-86 16 US-10-775-640-12	12 US-10-239-656-3 12 US-10-239-656-2 12 US-10-239-656-9 12 US-10-772-012-836 12 US-10-772-012-836 14 US-10-226-420-11 15 US-10-335-009-6
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ALIGNMENTS

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Patent No. US20020155110A1

Patent No. US20020155110A1

APPLICANT: GENINI SCIENCE, INC.

APPLICANT: Takahashi, No. US20020155110Aluaki

TITLE OF INVENTION: PHARMACHUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THE FILE REFERENCE: 021286/0278719

TITLE OF INVENTION: UNDER: 05/09/811,367B

CURRENT APPLICATION NUMBER: 60/190,716

PRIOR APPLICATION NUMBER: 60/190,716

PRIOR FILING DATE: 2000-03-17

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NO 3
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100.0%; Pred. No. 7.9e-101;
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Best Local Similarity 100.
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85 HCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID---GW 141
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                                                                                                                                                                                        85 HCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID---GW 141
                                                                                                                                                                                                                                     71 NCYFISSEQKTWNESRHLCASQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEEHTAW 128
                                                                                                                                      14 GTLGIİCLİMATLGİLLKNİFTKLSIEPAFTPGPNIELQKDSDÜ--Ü-SÜQEKMVGYRC 70
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APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Kelleher, Kerry S.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----KDSTCSHCPSCPILWTRNGS
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                                                                                              KDSTCSHCPSCPILWTRNGS
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                                                                                                                                                                                                                                                                                         142 RWEGGPALSLRILTN---SLIQRCGAIHRNG-LQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/10335009
Publication No. US20040001804A1
GENERAL INFORMATION:
APPLICANT: Portunelloor, Mathew A.
TITLE OF INVENTION: LLT USES THEREOF IN IMMUNE SYSTEM MODULATION
FILE REFERENCE: 11707.02/469687-7
CURRENT APPLICATION NUMBER: US/10/335,009
CURRENT FILING DATE: 2002-12-31
FRIOR APPLICATION NUMBER: US 09/475,365
PRIOR FILING DATE: 10399-12-30
                                                 31;
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  DB 10; Length 179;
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                                               68; Indels
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Pred. No. 1.3e-10;
                           Pred. No. 1.3e-10;
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31.8%; Pred. No. ...
17; Mismatches
                                               17; Mismatches
  17.3%; Score 178.5;
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                                                                                                 44 GLLTVILMSLLMYQRILCCGS---
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APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
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APPLICANT: Treacy, Maurice
APPLICANT: Bowman, Michael R.
                           31.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 17.35
Best Local Similarity 31.85
Matches 54; Conservative
                                                    54; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
Query Match
Best Local Similarity
Matches 54; Conserv
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US-10-335-009-10
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US-10-114-893-22
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APPLICANT: GEMINI SCIENCE, INC.
APPLICANT: Takahashi, No. US20020155110Aluaki
APPLICANT: Takahashi, No. US20020155110Aluaki
APPLICANT: Mikayama, Toshifuni
TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
TITLE OF INVENTION: PHARMACETTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THEM FILE REFERENCE: 021286/0278719
CURRENT APPLICATION NUMBER: 03/09/811,367B
PRIOR PAPLICATION NUMBER: 60/190,716
PRIOR APPLICATION NUMBER: 60/190,716
PRIOR APPLICATION NUMBER: 60/190,716
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TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REFERENCE: PA-0035 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 838; DB 9;
; Pred. No. 1.4e-80;
15; Mismatches 21;
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CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 130
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Publication No. US20030108871A1
GENERAL INFORMATION:
                                                                                                                                                                                                    Sequence 5, Application US/09811367B Patent No. US20020155110A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
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80.7%;
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ORGANISM: Homo sapiens
FEATURE:
                                  WICKKVLY 188
                                                                               181 WICKKVLY 188
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Best Local Similarity
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US-09-919-039-130
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FILE REFERENCE: PTZ14C1
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                                                                                                                                                                                                                                                                                                                                                              -CPILWTRNGSHCYYFSMEKKDWN 97
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                                                                                                                                                                                                                                                                                                                      29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 310, Application US/09764870

Patent No. US20020042386A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PT214

CURRENT APPLICATION NUMBER: US/09/764,870

CURRENT APPLICATION NUMBER: US/09/764,870

CURRENT PILING DATE: 2001-01-17

PATOT APPLICATION ARE REMOVED - CONSULT PALM OF file wrapper
NUMBER OF SEQ ID NOS: 646

SOFTWARE: PATENTIN VET. 2.0
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                                                                                                                                                                                                                                                                                                                    67; Indels
                                                                                                                                                                                                                                                                            ch 15.6%; Score 160.5; DB 13; Similarity 26.8%; Pred. No. 1e-08; 42; Conservative 19; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 LSLRILTNSLIQRCGAIHRNGLQASSCEVALQWICKK 185
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FILE REFERENCE: GI 6000-10A
CURRENT APPLICATION NUMBER: US/10/114,893
CURRENT FILING DATE: 2002-04-02
FARLIER APPLICATION NUMBER: 09/413,232
FARLIER FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 321
SEQ ID NO 22
LENGTH: 181
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; ORGANISM: Homo sapiens
US-10-114-893-22
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US-09-764-870-310
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Best Local Similarity
Matches 42; Conserv
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Best Local Similarity
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US-09-764-870-310
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US-10-125-540-310
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LENGTH: 182
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60 LCCG-SKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                   Length 182;
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CURRENT APPLICATION NUMBER: US/10/125,540
CURRENT FILING DATE: 2002-04-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 310
LENGTH: 182
                                                                                                                                                                                                                               15.2%; Score 156; DB 14; ilarity 29.2%; Pred. No. 3.1e-08; Conservative 18; Mismatches 59;
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PRIOR FILING DATE: 2000-01-07
PRIOR PILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
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PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 1995-09-10
PRIOR FLING DATE: 1995-09-10
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR FILING DATE: 2000-06-23
PRIOR PRIOR DATE: 1999-10-19
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Publication No. US20030022279A1
GENERAL INFORMATION:
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Fraser, Christopher C
Sharp, John D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 NGLQASSCEVALQWICK 184
                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 40; Conserv
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US-09-759-130B-98
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US-10-741-790-98
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LENGTH: 94
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APPLICANT: Myes's Paul S
APPLICANT: Wrighton, Nicolas
APPLICANT: Wrighton, Nicolas
APPLICANT: Geiby, Kevin R
APPLICANT: Geodarl, Andrew
APPLICANT: Goodarl, Andrew
APPLICANT: Goodarl, Andrew
APPLICANT: Goodarl, Andrew
APPLICANT: GOODARD: GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: USES.
TITLE OF INVENTION: USES.
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TITLE OF INVENTION: USES.
TITLE OF INVENTION: USES.
TITLE OF INVENTION: UNMERR: US 09/479, 249
PRIOR FILING DATE: 2000-01-07
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR PELING DATE: 1999-06-14
PRIOR PELING DATE: 1999-06-19
PRIOR APPLICATION NUMBER: US 09/393, 996
PRIOR APPLICATION NUMBER: US 09/393, 996
PRIOR APPLICATION NUMBER: US 09/393, 996
PRIOR APPLICATION NUMBER: US 09/393, 996
PRIOR APPLICATION NUMBER: US 09/420, 707
PRIOR APPLICATION NUMBER: US 09/420, 707
PRIOR APPLICATION NUMBER: US 09/420, 707
PRIOR APPLICATION NUMBER: US 09/420, 707
PRIOR APPLICATION NUMBER: US 09/420, 707
PRIOR APPLICATION NUMBER: US 09/420, 707
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PRIOR APPLICATION NUMBER: US 09/420, 707
PRIOR APPLICATION NUMBER: US 09/420, 707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 SESSWNESRDFCKGKGSTLAIVNTPEKLKFLQDITDAEKYFIGLIYHREEKRWRWINNSV 124
                                                                                                                                                                                                                                                                                                                                       40 MVALGLLTVIL----MSL-LMYQRILCCGSKD---STCSHCPSCPILWTRNGSHCYYFSM 91
                                                                                                                                                                                                                                                                                                                                                                                                5 MIISGLIVVVLKVVGMTLFLLYFPQIFNKSNDGFTTTRSYGTVCPKDWEFYQARCFFLST 64
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                           Indels 18;
                                                                                                                                                                                                                   15.0%; Score 154; DB 10; Length 165; 28.6%; Pred. No. 4.5e-08; tive 26; Mismatches 71; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 98 LENGTH: 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals,
APPLICANT: McCarthy, Sean A
APPLICANT: Fraser, Christopher C
APPLICANT: Sharp, John D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 98, Application US/10741790 Publication No. US20040121396A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barnes, Thomas S
Kirst, Susan J
Mackay, Charles R
Myers, Paul S
Leiby, Kevin R
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Best Local Similarity 28.64
Matches 46; Conservative
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ORGANISM: Homo sapiens
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US-09-759-130B-98
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US-10-741-790-98
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 FGEYLGODFYWIGLRNIDG--WRWEGGPALSLRILTNSLIORCGAIHRNGLQASSCE--V 177
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                                                                                                                                                                                                            92 EKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGL---RNIDGWRWEGGPA 148
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                                                                                                      40 MVALGLLTVIL----MSL-LMYQRILCCGSKD---STCSHCPSCPILWTRNGSHCYYFSM 91
                                                                                                                                         8; Gaps
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TITLE OF INVENTION: LLT USES THEREOF IN IMMUNE SYSTEM MODULATION
FILE REFERENCE: 11707.02/469687-7
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Betent No. US20020042386A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PT214
CURRENT RELIANG DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 646
SOFTWARE: PatentIN Ver. 2.0
     Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 132;
                                                       71; Indels
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                                                                                                                                                                                                                                                                                                                       149 LSLRILINSLIQRCGAIHRNGL----QASSCEVALQWICKK 185
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Best Local Similarity 28.9%; Pred. No. 7.1e-08;
Matches 37; Conservative 17; Mismatches 66;
15.0%; Score 154; DB 16; 28.6%; Pred. No. 4.5e-08; iive 26; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/335,009
CURRENT FILING DATE: 2002-12-31
PRIOR APPLICATION NUMBER: US 09/475,365
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
US-10-335-009-4
Sequence 4, Application US/10335009
Publication No. US20040001804A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Porunelloor, Mathew A. APPLICANT: Boles Kent S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.2
                                                       Conservative
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     Query Match
Best Local Similarity
Matches 46; Conserv
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69 CSHCPS-CPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLG 127

Gaps

3;

Indels

64;

Score 148.5; DB 9 Pred. No. 1.4e-07; 3; Mismatches 64

14.4%; Scol 26.2%; Pred tive 23;

Query Match
Best Local Similarity 26.2%
Matches 32; Conservative

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Gaps

ORGANISM: Homo sapiens

TYPE: PRT

; UKGAN15: 110.... US-09-764-870-340

DB 9; Length 140;

Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 340
LENGTH: 140

187 LY 188 AY 139 APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ14
CURRENT APPLICATION NUMBER: US/09/764,870
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patentin Ver. 2.0

Sequence 486, Application US/09764870; Patent No. US20020042386Al; GENERAL INFORMATION:

RESULT 14 US-09-764-870-486

128 QDFYWIGLRNI-DGWRWEGGPALSLRILTNSLIQRCGAIHRNGLQASSCEVALQWICKKV 19 CIKCEAPCPEDWLLYGRKCYFFSEEPRDWNTGRQYCHTHEAVLAVIOSQKELEFMFKFTR

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FEATURE:
NAME/KRY: SITE
LOCATION: (52)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                             ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-870-466
                                                                                                                                                                                                                                                                                                                                                                                    70 SHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQD 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 SHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQD 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (68) — A OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino US-10-125-540-466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Nucleic Acids, Proteins, and Anti-
FILE REFERENCE: PTZ14C1
CURRENT APPLICATION VMBER: US/10/125,540
CURRENT Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patentin Ver. 2.0
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36.2%; Pred. No. 8.7e-08;
tive 10; Mismatches 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 FYWIGL--RNIDG-WRWEGG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 YYWXGLTDRGTEGSWRWTDG 84
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1 Similarity 36.2%;
29; Conservative 10
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Best Local Similarity
Matches 29, Conserva
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Best Local Similarity
Matches 29; Conserva
                                                                                                                                                                                                        NAME/KEY: SITE
LOCATION: (68)
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69 CSHCPS-CPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLG 127
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                                                                                                                                                                                        19 CIKCEAPCPEDWLLYGRKCYFPSEEPRDWNTGRQYCHTHEAVLAVIQSQKELEFMFKFTR 78
                                                                                     Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Antibodies
                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and AntiFILE REFERENCE: P7214C1
CURRENT APPLICATION NUMBER: US/10/125,540
CURRENT FILING DATE: 2002-04-19
Prior Application removed - See File Wrapper or Palm
                                                                                   DB 9;
                                                                               14.4%; Score 148.5; DB 9 26.2%; Pred. No. 1.4e-07; iive 23; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 340, Application US/10125540 Publication No. US20030059875A1 GENERAL INFORMATION:
                                                                                                                        32; Conservative
               ORGANISM: Homo sapiens
                                                                                                Best Local Similarity
Matches 32; Conserv
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                                      US-09-764-870-486
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TYPE: PRT
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130 FYWIGL--RNIDG-WRWEGG 146

qq à 65 YYWXGLTDRGTEGSWRWTDG 84

APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PTZ14
CURRENT APPLICATION NUMBER: US/09/764,870
CURRENT FILING DATE: 2001-01-17

Sequence 340, Application US/09764870 Patent No. US20020042386A1 GENERAL INFORMATION:

RESULT 13 US-09-764-870-340

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Search completed: August 10, 2004, 16:53:37
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                                                                                                                                                                                                                                                                                                                                                                                    1 MADSSIYSTLELPEAPQVQD......GLQASSCEVALQWICKKVLY 188
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4: /cgn2_6/ptcdata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/2/iaa/pcTUS_COMB.pep:*
6: /cgn2_6/ptcdata/2/iaa/pcTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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PCT-US95-04258-5
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US-08-69-095-9
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US-08-68-342-3
US-08-650-578-2
US-09-113-788-3
US-09-113-788-3
US-09-113-789-9
US-08-722-126A-9
PCT-US95-04258-9
US-08-543-246B-19
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US-08-772-440-31
US-08-772-440-31
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US-08-722-126A-10
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Listing first 45 summaries
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                                                                                                                               protein search, using
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Match Length
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seq length: 188
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Sequence 21, Ap. Sequence 16, App. Sequence 18, App. Sequence 18, App. Sequence 2, App. Sequence 2, App. Sequence 2, App. Sequence 4, App. Sequence 167, App. Sequence 167, App. Sequence 6, App. Sequence 6, App. Sequence 17, App. Sequence 17, App. Sequence 17, App. Sequence 17, App. Sequence 17, App. Sequence 17, App. Sequence 17, App. Sequence 17, App. Sequence 17, App. Sequence 17, App. Sequence 17, App. Sequence 17, App. Sequence 17, App. Sequence 17, App. Sequence 17, App. Sequence 17, App.	S DING A MAST CELL ANTIGEN (MAFA) C: 300 ion #1.30
4 US-09-531-056A-21 4 US-09-531-056A-15 4 US-09-531-056A-18 1 US-08-531-056A-18 1 US-08-294-859-2 1 US-08-294-859-2 1 US-08-294-859-2 1 US-08-81-676-2 1 US-08-93-929A-4 4 US-09-489-847-167 4 US-09-489-847-167 5 US-09-489-847-326 6 DCT-US92-10344-6 5 PCT-US92-10344-6 5 DCT-US92-10344-6 5 DCT-US92-10344-6 5 US-08-893-928-6 6 DCT-US92-10344-6 7 US-08-893-928-6 8 US-08-772-440-17 9 US-08-772-440-17 9 US-08-772-440-17	IGNMENT: LE ENCOI P.L.L.(', Ste. 126A 1258
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127 127 127 127 127 127 127 127 127 127	TULT 1 08-722-126A-5 CACHERAL INFORMATION: APPLICANT: BECHT, ISTA APPLICANT: GUTHANN, MAPLICANT: TAL, Michae TITLE OF INVENTION: A TITLE OF INVENTION: A TITLE OF INVENTION: A TITLE OF INVENTION: A TITLE OF INVENTION: A TITLE OF INVENTION: A TITLE OF INVENTION: A TITLE OF INVENTION: A TITLE OF INVENTION: A TITLE OF INVENTION: A TITLE OF INVENTION: A TITLE OF INVENTION: A TITLE OF INVENTION: A TITLE OF INVENTION AND STREET: 419 Seventh CITY: Washington STREET: D.C. COUNTRY: UNITED STAT ZIP: 20004 COMPUTER: IBM PC COM OPERATING SYSTEM: PC COMPUTER: BACOMPY APPLICATION NUMBER: TILING DATE: 08-APR- APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: REGISTRATION NUMBER:
2	RESULT 1 US-08-722-126 SEGUETIC 5. FACTOR 10 APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN COMPUT COMP

Score 838; DB 3; Length 188; Pred. No. 1.8e-86;

81.48; 80.78;

Query Match Best Local Similarity

18, 17, 22, 19,

Sequence Sequence Sequence

US-08-543-246B-20 US-08-772-440-10 US-08-543-246B-18 US-08-543-246B-17 US-09-531-056A-22 US-09-531-056A-19

Sequence Sequence Sequence

Sequence Sequence

Sequence

LENGTH: 188 amino acids; TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein US-08-722-126A-5

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75 CPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIG 134
121 LFGEYLGQDFYWIGLRNIDGWRWEGGPALSLRILTWSLIQRCGAIHRNGLQASSCEVALQ 180
                       1 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIG
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                                                                                                                                                                                                                                                                                        APPLICANT: GUTHMANN, Marcelo D.
APPLICANT: GUTHMANN, Marcelo D.
APPLICANT: TAL, Michael
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
NUMBER OF SEQUENCES: 20
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: BACENII Release #1.0, Version #1.30
SOGTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,126A
FILING DATE: 08-0CT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWNY ROGET L.
NAME: BROWNY ROGET L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 551; DB 3;
Pred. No. 2e-54;
                                                                                                                                                                                                                                                                                                                                                                                                      AUDRESSEE: BROWDY AND NEIMARK, P.L.L.C. STREET: 419 Seventh Street N.W., Ste. 300 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UNITED STATES OF AMERICA ZIP: 20004
                                                                                                                                                                                                                             Sequence 6, Application US/08722126A Patent No. 6034227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PECH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEPHONE: (202) 737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 53.5%;
1 Similarity 84.1%;
95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
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WICEKVL 187
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STRANDEDNESS: Si
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Best Local Similarity
                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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PCT-US95-04258-6
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US-08-722-126A-6
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                                                                                                                                                        61 CCGSKGFMCSQCSRCPNLMMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLFFPDNQGVN 120
                                                                                                                                                                                                                                        CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120
                                             1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLITVILMSLLMYQRIL 60
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                                                                       1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGELTVILMSLLLYQRTL
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        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPATIBLE
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCTUS95/04258
FILING DATE: 06-APR-1995
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
      21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A DNA MOLECULE ENCODING A MAST CELL FUNCTION-ASSOCIATED ANTIGEN (MAFA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application PC/TUS9504258 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PECH.
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEFX: 202-737-3528
        15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 248633
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amirror
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: A DNA TITLE OF INVENTION: FUNCTION FORMER OF SEQUENCES: 10 CORRESPONDENCE ADDRESSE: ADDRESSE: ADDRESSE: BROWDY AND NI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 2
          151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein PCT-US95-04258-5
                                                                                                                                                                                                                                                                                                                          181 WICEKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 419 Sevent CITY: Washington STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                              WICKKUL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US95-04258-5
                                                                                                                                  61
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        Matches
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                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84
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                                                                                                                         1 PSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDSTCSHCPSCPILMTRNGS
                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 RWEGGPALSLRILTN---SLIQRCGAIHRNG-LQASSCEVALQWICKKVL 187
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         25.9%; Score 267; DB 4; Length 76; 59.5%; Pred. No. 1.2e-22; tive 10; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hillman, Jennifer L.
APPLICANT: Au-Young, Janice
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 17.3%; Score 178.5; DB 1; 1 Similarity 31.8%; Pred. No. 3.5e-12; 54; Conservative 17; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTY: U.S.

ZIE: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,095
FILING DATE: Fled Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                         ; Sequence 9, Application US/08690095; Patent No. 5792648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 GLLTVILMSLLMYQRILCCGS
                                                                                                                                                                                    133 IGLRNIDGWRWEGG 146
                                                                                                                                                                                                                                61 IGLRNMSGWRWEDG 74
      Query Match
Best Local Similarity 59.5*
Matches 44; Conservative
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Best Local Similarity
Matches 54; Conserva
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LIBRARY: General
AND: 1098617
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                                                                                                                                                                                                                                                                                                                       US-08-690-095-9
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Patent No. 645563
GERRAL INFORMATION:
GESTIVE SET Existol-Wyers Squibb Company
TITLE OF INVENTION: DAM MOLECTLES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUSI
TITLE OF INVENTION: PROTEINS
FILE REPERBACE: DB20 NPF
CURRENT APPLICATION NUMBER: US/09/531,056A
CURRENT FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.0
SEQ ID NO 23
LENGTH: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 CPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIG 60
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Pred. No. 2e-54;
9; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PACEDALIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
ATTORNEY/AGBNT INFORMATION:
NAME: BROWDY, ROGER L.
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
                                                                  A DNA MOLECULE ENCODING A MAST CELL FUNCTION-ASSOCIATED ANTIGEN (MAFA)
                                                             TITLE OF INVENTION: A DNA MOLECULE ENCODING A MATITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN NUMBER OF SEQUENCES: 10
CORRESSED ANDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Mashington
STATE: D.C.
Sequence 6, Application PC/TUS9504258
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 53.5%;
Best Local Similarity 84.1%;
Matches 95; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PCT-US95-04258-6
                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ORGANISM: Homo sapiens
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STRANDEDNESS: si
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 NCYFISSEQKTWNESRHLCASQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEEHTAW 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KDSTCSHCPSCPILWTRNGS 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 17.3%; Score 178.5; DB 2; Length 179; Best Local Similarity 31.8%; Pred. No. 3.5e-12; Matches 54; Conservative 17; Mismatches 68; Indels 31.
                                                                         GENERAL INFORMATION:
APPLICANT: Chang, Chiwen
APPLICANT: Aramburu Beltran, Jose
APPLICANT: Lopez-Botet, Miguel
APPLICANT: Lopez-Botet, Miguel
APPLICANT: Lanier, Lewis L.
APPLICANT: Lanier, Lewis L.
TITLE OF INVENTION: Purified Mammalian NK Antigens and TITLE OF INVENTION: Related Reagents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,578
                                                                                                                                                                                                                                        STREET: 901 California Avenue CITY: Palo Alto COUNTRY: USA ZID: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,339
FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBB PC compatible
OPBRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08688342
Patent No. 5871964
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Gocks, Benjamin G.
APPLICANT: Goli, Surya K.
                                    Sequence 2, Application US/08650578 Patent No. 5811284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 GLLTVILMSLLMYORILCCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 179 amino acids
amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-08-688-342-3
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RESULT 7
US-08-650-578-2
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85 HCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID----GW 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -KDSTCSHCPSCPILWTRNGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 LWENGSALSQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQQL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.3%; Score 178.5; DB 2;
31.8%; Pred. No. 3.5e-12;
tive 17; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: AL-Young, Janice
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FASTERO VESSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/68,342
FILING DATE: F11ed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-0095-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-485-0555
ITELEPHONE: 415-485-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                              ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-113-788-3; Sequence 3, Application US/09113788; Patent No. 5969104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 GLLTVILMSLLMYQRILCCGS--
                                                                                                                                                                                                              ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 179 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 31.8
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94304
COMPUTER READABLE FORM:
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STATE: CA
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-688-342-3
                                                                                                                                            CITY: P
STATE:
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85 HCYYFSMEKKDWNSSLKFCADKGSHLLIFPDNQGVKLFGEYLGQDFYWIGLRNID---GW 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 GTLGIICLSLMATLGILLKNSFTKLSIEPAFTPGPNIELQKDSDC--C-SCOEKWVGYRC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----KDSTCSHCPSCPILWTRNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 RWEGGPALSLRILIN---SLIQRCGAIHRNG-LQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 LWENGSALSQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQQL 178
                                                                                                                                                                                                                                                                                                                                                                                             ch 17.3%; Score 178.5; DB 3; Length 179; 1 Similarity 31.8%; Pred. No. 3.5e-12; 54; Conservative 17; Mismatches 68; Indels 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/08722126A
Patent No. 603427
GENERAL INFORMATION:
APPLICANT: BECHT, Israel
APPLICANT: TAL, Michael
ITILE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
ITILE OF INVENTION: PUNCTION-ASSOCIATED ANTIGEN (MAFA)
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.30
                                                                                     PF-0110 US
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APPLICATION NUMBER: US/08/722,126A
FILING DATE: 08-OCT-1996
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                           REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 GLLTVILMSLLMYQRILCCGS-
                        ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/1
FILING DATE: 06-APR-1995
                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                      GenBank
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LIBRARY: Gell.
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                                                                                                                                                                                                                                                         TOPOLOGY: lin
        FILING DATE:
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US-08-722-126A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 IWENGSALSQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQQL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
AITLE Of Oli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
NUMBER OF SEQUENCES: 9
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.3%; Score 178.5; DB 2
31.8%; Pred. No. 3.5e-12;
tive 17; Mismatches 68
                                                                                                                                                                                                                                                         PF-0095-1 CIP
                                                                                               APPLICATION DATA:
FILING DATE:
PRIOR APPLICATION NUMBER: 08/688,342
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-009F
TELECOMMUNICATION INFORMATION:
TELEPANE: 415-855-0555
TELEPANE: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
TEMPORATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                             US/09/113,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SUSTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/113,789
                  FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/690,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/09113789
Patent No. 6034219
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 GLLTVILMSLLMYQRILCCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54; Conservative
Diskette
                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 31.7
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Matches 54; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIALL
LIBRARY: General Towns: 1098616
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MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-113-788-3
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31;

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14.8%; Score 152; DB 5; Length 122; 27.9%; Pred. No. 2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: PECHT, Israel
APPLICANT: GUTHARNN, Marcelo D.
APPLICANT: TAL, Michael
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAPA)
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,126A
FILING DATE: 08-0CT-1996
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1955
PRIOR APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.6%; Score 150.5; DB 3; 26.3%; Pred. No. 2.8e-09; tive 20; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUDKESSEE: BROWDY AND NEIMARK, P.L.L.C. STREET: 419 Seventh Street N.W., Ste. 300 CITY: Washington STATE: D.C.
                                             22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D.C. COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08722126A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PECHT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 26.3%
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                               34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sil
    Query Match
Best Local Similarity
Matches 34; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6034227
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                187 LY 188
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US-08-722-126A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 IGLRYTLPDMNWKWINGSTLNSDVLKITGDTENDSCAAISGDKVTFESCNSDNRWICQKE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 IGLRNI---DGWRWEGGPALS---LRILINSLIQRCGAIHRNGLQASSCEVALQWICKKV 186
                                                                                                                                                                                                                                                                                                                                                                                                          1 CPQDWLSHRDKCFHVSQVSNTWEEGLVDCDGKGATLMLIQDQEELRFLLDSIKEKKNSFW 60
                                                                                                                                                                                                                                                                                                                                      Gaps
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&
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application PC/TUS9504258
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
TITLE OF INVENTION: PUNCTION-ASSOCIATED ANTIGEN (MAFA)
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: AL9 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06.APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FILING DATE: 08.APR-1994
ATTORNEY/ARGHT INCOMPATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PECHT=1 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-737-3528
TELEFAX: 202-737-3528
           REFERENCE/DOCKET NUMBER: PECHT=1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
                                                                                                                                                                                 single
                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
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75 CPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGBYLGQDF--YW 132
                                                                              133 IGLRNI---DGWRWEGGPALS---LRILTNSLIQRCGAIHRNGLQASSCEVALQWICKKV 186
                                                                                                        61 IGLRYTLPDMNWKWINGSTLNSDVLKITGDTENDSCAAISGDKVTFESCNSDNRWICQKE 120
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135 LRNIDG--WRWEGGPALSLRI-LTNSLIQRCGAIHRNGLQASSCEVALQWICKK 185
                                    61 LKKEPGHPWKWSNGKEFNNWFNVTGS--DKCVFLKNTEVSSMECEKNLYWICNK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
RAPPLICATION NUMBER: II 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59; Indels
                                                                                                                                                                                                          A DNA MOLECULE ENCODING A MAST CELL FUNCTION-ASSOCIATED ANTIGEN (MAFA)
                                                                                                                                                        TITLE OF INVENTION: A DNA MOLECULE ENCODING A M. TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEB: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.6%; Score 150.5; DB 5 26.3%; Pred. No. 2.8e-09; Live 20; Mismatches 59
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Patent No. 6262244
GENERAL INFORMATION:
PAPLICANT:
TITLE OF INVENTION: natural killer of WINGHER SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                             Sequence 8, Application PC/TUS9504258 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 25,618 REFERENCE/DOCKET NUMBER: PECTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Michael W. Glynn
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LENGTH: 115 amin.
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TELEFAX: 202-737-3528
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amino acid
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MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
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US-08-543-246B-19
                                                                                                        RESULT 14
PCT-US95-04258-8
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71 HCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDF 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 HCGHCPEEWITYSNSCYYIGKERRIWEESLLACTSKNSSLLSIDNERRIKFLASILPSS-
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                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN REGEASE #1.0, Version #1.30 (EPO)
APPLICATION NUMBER: US/08/543,246B
FILING DAFE:
                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,663
FILING DATE: 28-MAR-1991
PRIOR APPLICATION NUMBER: US 07/676,663
FILING DATE: 28-MAR-1992
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/122,514
FILING DATE: 24-SEP-193
ATTORNEY,AGENT INFORMATION:
NAME: KASSENOFF, MALVYN M.
REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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  No. 6262244artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: August 10, 2004, 16:45:20 Job time : 15.5 secs
                     564 Morris Avenue
                                                                                                                                                              Floppy disk
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Best Local Similarity 28.9%
Watches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 908-522-6955
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
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MOLECULE TYPE: protein
HYDOTHETICAL: NO
                                                                                          COUNTRY: US
ZIP: 07901-1027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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  Abba.
STREET: Summit,
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ADDRESSEE:
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5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2004
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- protein search, using sw model OM protein Run on:

August 10, 2004, 16:39:40; Search time 13.5 Seconds (without alignments) 1339.556 Million cell updates/sec

US-09-811-367B-5

1 MADNSIYSTLELPAAPRVQD.......GLHASSCEVALQWICEKVLP 188 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

95185

length: 188 Minimum DB seq length: 0 Maximum DB seq length: 18 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. score

	G	mast cell function	ral ki		2	hepatic lectin hom	alpha		botrocetin alpha c	botrocetin beta ch		coadulation factor	agkisacutacin alph	hepatic lectin hom	lectin BRA3-2 pred			pancreatitis-assoc	coaqulation factor	regenerating islet	pancreatic stone p		lectin, galactose-	pancreatic stone n	echicetin beta cha	Coadulation factor		- 1	red II. redenerati	pancreatitis-assoc
SUMMARIES	ID	I59421	T28140	T28141	JC7135	WMVZF2	PC7027	JC4691	A47267	B47267	JC7105	B42972	JC7134	WMVZF8	LNRC3	LNRC1	S78774	A49616	JC4329	RGHU1A	A45751	JC5059	A38609	A28351	JC2415	JC4690	RGHU1B	529822	B47148	S54979
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æ	Query	100.0	15.7	15.3	14.1	13.2	13.0	٠	•			11.1	11.1			٠	10.5	10.0	6.6	•	٠		•		9.3				9.1	
	Score	1036	162.5	158	146	137	134.5	127.5	126	123.5	121.5	115	114.5	113	112.5	112	108.5	103.5	102.5	102	102	100.5	100	98	96.5	96.5	95	94.5	94	92.5
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pancreatic stone p	antilleeze protein bitiscetin alpha c	pancreatic thread	type II antifreeze	hypothetical prote	lectin - barnacle	tokaracetin beta c	echinoidin - sea u	red I, redeneratin	antifreeze protein	ovocleidin - chick	hepatic lectin hom	regenerating profe	hypothetical prote	alboaggregin-B alp
A41719	JC5058	A37194	JC7938	T21396	S10548	S56007	A26697	A47148	JH0626	S78596	WMVZEL	183377	T28809	B56829
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80 m	9.9	8.5	8.4	4.	8.4	8.3	8.2	7.9	7.9	7.9	7.9	7.6	7.6	7.4
92	89.5	88	87	87	87	86	85	82	82	81.5	81.5	79	78.5	77
31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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C;Accession: 159421
R;Guthmann, M.D.; Tal, M.; Pecht, I.
Proc. Natl. Acad. Sci. US. A. 92, 9397-9401, 1995
A;Title: A secretion inhibitory signal transduction molecule on mast cells is another of A;Reference number: 159421; MUID:96016176; PMID:7568140
A;Accession: 159421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120
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                                                                                    mast cell function associated antigen - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1036; DB 2;
100.0%; Pred. No. 3.2e-90;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.0%; Pr
Matches 188; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 WICEKVLP
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RESULT 1
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9 9

RESULT 2

Jobesties: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T28140
R;Milne, S:; Kaufman, J:; Beck, S.
submitted to the EMBL Data Library, May 1998
A;Reference number: 220475
A;Reference number: 220475
A;Reference number: 220475
A;Accession: T28140
A;Status: preliminary; translated from GB/EMBL/DDBJ

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C;Species: fowlpox virus
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jun-2000
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jun-2000
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jun-2000
C;Accession: B9963
B;Tomley, F; Binns, M.; Campbell, J.; Boursnell, M.
A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlpo A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlpo A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlpo A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlpo A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlpo A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlpo A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlpo A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlpo A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlpo A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlpo A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlpo A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlpo A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlpo A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-terminal, near-
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C;Species: Calloselasma rhodostoma (Malayan pit viper)
C;Date: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change O2-Jun-2000
C;Date: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change O2-Jun-2000
R;Chacession: PC7027
R;Chung, C.H.; Au, L.C.; Huang, T.F.
B;Chung, C.H.; Au, L.C.; Huang, T.F.
B;Chung, C.H.; Au, L.C.; Huang, T.F.
A;Atitle: Molecular cloning and sequence analysis of aggretin, a collagen-like platelet A;Reference number: PC7027; MUID:99443731; PMID:10512747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 SLKFCAD--KGSHLLTFPDNQG----VNLFQEYVGEDFYWIGLRDI-DG--WRWEDGPAL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 DWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSIL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 NWNDSKKLCDVMDSSLIRFDNIETLNFVSRY-GKGSYWI---DINQNRKIPGINF$L-YY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - fowlpox virus (isolate HP-438[Munich])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 VSYLVMVALGLLIVILMSLLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 VSCYALTVLGILCLILFTILV---VVTCKWYYAFPYFSKVCPDEWIGYNSKCYYFTINET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 VMVALGLITVILMSLLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----LSGTAADCPSEWSSYEGHCYKPFDEPKTWAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                            A;Accession: PC7038
A;Molecule type: protein
A;Residues: 24-50;59-83;102-107;112-114 <CH2>
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; heterodimer; venom
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-146/Product: agkisacutacin beta chain #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 167;
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1 Similarity 29.1%; Pred. No. 1.2e-05;
44; Conservative 21; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 146; DB 2;
Pred. No. 1.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 EQGVNDICLLFDTSNIIEMSCIFHERTICVK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DYKDWREQFECLUSRIVNNEWLSMDCGT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -SLSILSNSVVQKCGT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 SNSVVQKCGTIHRCGLHASSCEVALQWICEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;49-152/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hepatic lectin homolog (BamHI-ORF2)
                                    A; Experimental source: venom gland
                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 14.1%;
1 Similarity 27.7%;
41; Conservative 1
A;Cross-references: GB:AF176421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 IFVSFGLLVVFLS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 44; Conserva
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Best Local S
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R/Milne, S.; Kaufman, J.; Beck, S.

R/Milne, S.; Kaufman, J.; Beck, S.

R/Milne, S.; Kaufman, J.; Beck, S.

R/Milne, S.; Kaufman, J.; Beck, S.

R/Milne, S.; Kaufman, J.; Beck, S.

R/Milne, S.; Kaufman, J.; Beck, S.

R/Milne, S.; Kaufman, J.; Beck, S.

R/Milne, S.; Kaufman, J.; Beck, S.

R/Milne, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman,
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C;Species: Agkistrodon acutus (sharp-nosed viper)
C;Species: Agkistrodon acutus (sharp-nosed viper)
C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 24-oct-2000
C;Accession: JC7135; PC7038
R;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
Biochem: Biophys: Res. Commun. 265, 530-535, 199
A;Title: Purification, characterization, and CDNA cloning of a new fibrinogenlytic venom A;Reference number: JC7134; MUID:20025379; PMID:10558903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 WIGLRDIDG----WRWEDGPALS--LSILSNSVVQKCGTIHRCGLHASSCEVALQWICEK 185
                                        A;Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292544; PIDN:CAA18960.1
A;Experimental source: clone cB12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 CSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFY 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 CLLCPOFWRLLGDRCYELSTEKGNWTQAKMKCENLOSQLAVLRKKAEEDHLQQMAGAEPV 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 WIGLR-DIDGWRWEDGPAL----SLSILSNSVVQKCGTIHRCGLHASSCEVALQWICE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type lectin, B locus - chicken
Species: Gallus gallus (chicken)
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 CAQCPFDWIGFRGKCYYFSEDESNWTSSQNNCSALGASLAVFDSAEDLSFTWRHKGSSPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                       Length 170;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                      A;Map position: 16
A;Note: Intron positions not resolved (incomplete sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agkisacutacin beta chain precursor - sharp-nosed viper
                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.3%; Score 158; DB 2; 27.5%; Pred. No. 1.2e-07;
                                                                                                                                                                                                                                                                                                                                                                ; Score 162.5; DB 2; Pred. No. 4.8e-08; 16; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                15.7%;
28.1%;
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 28.1%
Matches 34; Conservative
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A,Map position: 16
A,Introns: 17/1; 74/3; 110/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-146 <CHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 K 185
                                                                                                                                                                                         A;Gene: B-NK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
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botrocetin alpha chain - jararaca
N'Alternate names: two chain botrocetin alpha chain
C'Species: Bothrops jararaca (jararaca)
C'Species: Bothrops jararaca (jararaca)
C'Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-May-1998
C'Accession: A47267; B37958
C'Accession: A47267; B37958
A'Y: Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.
Proc. Natl. Acad. Sci. U.S.A. 90, 928-932, 1993
A'Fitle: Primary structure of two-chain botrocetin, a von Willebrand factor modulator phase and a structure of two-chain botrocetin, a von Willebrand factor modulator phase and a structure of two-chain botrocetin.
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A,Molecule type: protein
A,Molecule type: protein
A,Molecule type: protein
A,Molecule type: none
A,Molecule type: Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Tritani, Trit
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R;Fujimura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Sus
Biochemistry 30, 1957-1964, 1991
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C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-May-1998
C;Dates: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-May-1998
C;Accession: B47267; C37958
R;Usami, Y:, Fulfiutura, Y:, Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.
Proc. Natl. Acad. Sci. U.S.A. 90, 928-932, 1993
A;Title: Primary structure of two-chain botrocetin, a von Willebrand factor modulator
A;Reference number: A47267; MUID:93157385; PMID:8430107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 CPSGWSSYEGNCYKFFQQKMWADAERFCSEQAKGGHLVS----IKIYSKEKDFVGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIKNIQSSDLYAWIGLRVENKEKQCSSEWSDGSSVSYENVVERTVKKCFALEK 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 1-40 <PUJ>
C;Complex: heterodimer of alpha and beta (see PIR:B47267) chains
C;Comperfamily: terranectin, C-type lectin homology
C;Keywords: hemagolutinin; heterodimer; venom
F;2-128/Domain: C-type lectin homology <LGH>
F;2-13,30-128,103-120/bisulfide bonds: #status experimental
F;80/Disulfide bonds: interchain (to beta-75) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 133;
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A,Residues: 1-40 <PUJ>
C.Complex: hetrordimer of alpha (see PIR:A47267) and beta chains
C,Superfamily: tetranectin; C-type lectin homology
C,Keywords: hemagglutinin; heterodimer; venom
--WRSRACRMMAQFVCE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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llarity 26.5%; Pred. No. 0.0001;
Conservative 24; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  botrocetin beta chain - jararaca
N/Alternate names: two chain botrocetin beta chain
                           108 LRYKAWAEESYCVYFKSTNNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 1-133 <USA>
A;Experimental source: venom
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Best Local Similarity
Matches 30; Conserv
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J. Biol. Chem. 266, 14903-14911, 1991
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J. Sill. Chem. 266, 14903-14911, 1991
J. Sill. Chem. 266, 14903-14911, 1991
J. R. Sill. Chem. 266, 14903-14911, 1991
J. R. Reference number: A3332; MUID:91332000; PMID:1831197
J. R. Residues: 24-146 ATO>
R. R. Residues: 24-146 ATO>
J. Biochem. 118, 965-973, 1995
J. Biochem. 118, 965-973, 1995
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A;Reference number: JC4329; MUID:96318509; PMID:8749314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coagulation factor IX/factor X-binding protein chain A precursor - habu
C;Species: Trimeresurus flavoviridis (habu)
C;Species: Trimeresurus flavoviridis (habu)
C;Species: Trimeresurus flavoviridis (habu)
C;Species: 16-Aug-1996 #sequence revision 16-Aug-1996 #text_change 20-Jun-2000
C;Accession: JC4691, B39322; JC4330
R;Matsuzaki, R.; Yoshiara, E.; Yamada, M.; Shima, K.; Atoda, H.; Morita, T.
Bjochem. Bjophys. Res. Commun. 220, 382-387, 1996
A;Title: cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant protein from A;Reference number: JC4690; MUID:96184662; PMID:8645314
A;Accession: JC4691
A;Molecule type: mRNA
A;Residues: 1-146 cMAII>
A;Cross-references: DDBJ:DB3332; NID:g1402641; PIDN:BAA11888.1; PID:g1402642
A;Access-references: DDBJ:DB3332; NID:g1402641; PIDN:BAA11888.1; PID:g1402642
                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                   ---OEY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 VGEDFYWIGLRDID-----GWRWEDGPALSLSILSNSVVQKCGTIHR-CGLHA---SSCE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 SLKFCADK--GSHLLIFPDNQGVNL----FQEYVGEDFYWIGLRDI----DGWRWEDGPA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDFGWSPYDQHCYQAFNEQKTWDEAEKFCRAQENGAHLASIESNGEADFVSWLISQKDEL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A. Accession: UC4330
A. Moclecule type: protein
A. Molecule type: protein
A. Molecule type: protein
A. Molecule type: protein
A. Molecule type: protein
A. Molecule type: protein
C. Keywords: anticoagulant; blood coagulation; lectin; venom
C. Keywords: anticoagulant; blood coagulation; lectin; venom
C. Keywords: anticoagulant; blood coagulation; lectin; venom
C. Keywords: factor IX/X binding predicted <SIG>
F:24-146/Product: factor IX/X binding predicted cMAT>
F:25-142/Domain: C-type lectin homology <LCH>
F:25-142/Domain: C-type lectin homology <LCH>
F:25-36,53-142,119-134/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 VMVALGLITVILMSLLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNS
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                          19;
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                                                                                                                                                                                                                                                                                                                                                                                                                     75 CPNLWMRNGSHCYYFSMEKRDWNSSLKFC--ADKGSHLLTFPDNQGVNLF---
                                                                                                                                                                                                                                                      Length 144;
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                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 L-----SLSILSNSVVQKCGTIHRCGLHASSCEVALQWICE 184
    A, Residues: 1-144 <CHU>
A, Experimental source: venom gland
C, Superfamily: tetranectin; C-type lectin homology
C, Keywords: disulfide bond; platelet aggregation; venom
                                                                                                                                                                                                                                        13.0%; Score 134.5; DB 2; 28.0%; Pred. No. 1.7e-05; ive 19; Mismatches 57;
                                                                                                                                                                                                   Query Match
Best Local Similarity 28.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 VALQWICEKVLP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 QMHAFVC-KLLP 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34; Conservative
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Matches 34; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
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NyAlternate names: fibrinogenlytic venom protein

NyAlternate names: fibrinogenlytic venom protein

C, Species: Agkistrodon acutus (sharp-nosed viper)

C, Species: Agkistrodon acutus (sharp-nosed viper)

C, Accession: UC7134; PC7037

C, Accession: UC7134; PC7037

E, Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.

Biochem: Biophys: Res. Commun. 265, 530-535, 1999

A, Title: Purification, characterization, and cDNA cloning of a new fibrinogenlytic veno A; Accession: UC7134

A; Molecule type: mRNA

A; Molecule type: mRNA

A; Molecule type: mRNA

A; Residues: 1-152 ccHEA

A; Accession: COMMUN gland

A; Accession: COMMUN gland

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CiSpecies: 40-69-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jun-2000
CiAccession: #12963
R:Tomley, F: Binns, M: Campbell, J: Boursnell, M.
J: Gen. Virol. 69, 1025-1040, 1988
A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlpc
A;Reference number: JT0442; MUD:88229622; PMID:2836548
A;Accession: #12963
A;Accession: #12963
A;Accession: H29963
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A;Accession: H2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 AESFCTKQVNGGHLVSIESSGEADFVAHLIAQKIKSAKIHVWIGLRAQNKEKQCSIEWSD 108
                                                                                                                                               75 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCAD--KGSHLLTFPDNQG----VNLFQEYVGE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 VMVALGLLIVILMSLLLYQRTLCCGSKGFMCSOCSRCPNLWMRNGSHCYYFSMEKRDWNS 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----LSGTAADCSSGWSSYEGHCYKVFKQSKTWAD 48
                                                                                                                                                                                               hepatic lectin homolog (BamHI-ORF8) - fowlpox virus (isolate HP-438[Munich])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:D00295; NID:g221380; PIDN:BAA00203.1; PID:g221394
C;Superfamily: fowlpox virus hepatic lectin homolog; C-type lectin homology
C;Keywords: early protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33;
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DB 2; Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPALSLSILSNSVVOKCGTIH-RCGLHASS---CEVALOWICE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;48-116/Domain: C-type lectin homology #status atypical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.1%; Score 114.5; DB 2;
21.5%; Pred. No. 0.0014;
tive 22; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Mosedues: 24-53;84-86;87-94;125-136;137-152 <CH2>
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; heterodimer; venom
                               , Pred. No. 0.001;
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.9%; Score 113;
11.1%; Score 115; 33.8%; Pred. No. 0.
                                                                                                                                                                                                                                                                                                               129 DEYWIGLRDIDGWRWED 145
                                                                                                                                                                                                                                                                                                                                                                              64 PATWIGL----GNMWKD 76
                                                                               26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                           Similarity
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Best Local Si
Matches 35,
       Query Match
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Matches 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aggretin beta chain - Malayan pit viper C;Species: Calloselasma rhodostoma (Malayan pit viper) C;Species: Calloselasma rhodostoma (Malayan pit viper) C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000 C;Date: 03-Dec-1999 #sequence_revision 07-105 R;Chung, C.H.; Au, L.C.; Huang, T.F. Biochem. Biophys. Res. Commun. 263, 723-727, 1999 Biochem. Biophys. Res. Commun. 263, 723-727, 1999 A;Title: Molecular cloning and sequence analysis of aggretin, a collagen-like platelet A;Reference number: PC7027, MOID:99443731; PMID:10512747
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R. Takeya, H.; Nishida, S.; Miyata, T.; Kawada, S.; Saisaka, Y.; Morita, T.; Iwanaga, S.
R. Takeya, H.; Nishida, S.; Miyata, T.; Kawada, S.; Saisaka, Y.; Morita, T.; Iwanaga, S.
J. Biol. Chem. 267, 14109-14117, 1992
A. Tile: Coaqulation factor X activating enzyme from Russell's viper venom (RVV-X). A I A; Reference number: A42972; MUID:92332516; PMID:1629211
A; Contents: V. r. siamensis
A; Accession: B42972
A; Accession: B42972
A; Accession: B42972
A; Residues: preliminary
A; Molecule type: protein
A; Residues: 1-123 craxx
A; Residues: 1-123 craxx
A; Residues: 1-123 craxx
C; Superfamily: tetranectin; C-type lectin homology
C; Reywords: hydrolase; metalloproteinase; venom; zinc
F; 4-121/Domain: C-type lectin homology cLCH>
F; 4-121/Domain: C-type lectin homology clcH>
F; 4-121/Domain: C-type lectin homology clcH>
F; 4-121/Domain: C-type lectin homology cLCH>
F; 4-121/Domain: C-type lectin homology cLCH>
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C;Date: 04-Mar_1993 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997
                                                                                                                                                                                                                                                                                                                   75 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADK--GSHLLTFPDNQGVNLFQEYVGE---- 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLKFC--ADKGSHLLTFPDNQG----VNLFQEYVGEDFYWIGLRDI---DGWRWEDGPAL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 AERFCKIQPKHSHIVSFQSAEEADFVVKITRPRIKANIVWMGISNIWHGCNWQWSDGARL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --LSGTGADCPSGWSSYEGHCYKPFNEPKNWAD 48
                                                                                                                                                                                                                                                                                                                                                                  2 CPPDWSSYEGHCYRFFKEWMHWDDAEEFCTEQQTGAHLVSFQSKEEADFVRSLTSEMLKG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 VMVALGLITVILMSLLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                           13;
               F;2-121/Domain: C-type lectin homology <LCH>
F;2-13,30-121,98-113/Disulfide bonds: #status experimental
F;75/Disulfide bonds: interchain (to alpha-80) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.7%; Score 121.5; DB 2; Length 146; 23.3%; Pred. No. 0.0003; ive 24; Mismatches 65; Indels 33
                                                                                                                                                                                                                                               Indels
                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLSILSNSVVQKCGTIHRCGLHAS----SCEVALQWICE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: mRNA
A,Residues: 1-146 <CHU>
A,Experimental Source: venom gland
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; platelet aggregation; venom
                                                                                                                                                               111.9%; Score 123.5; DB 2;
31.3%; Pred. No. 0.00016;
iive 12; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 DFYWIGLRDIDGW-----RWEDG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVVWIGLSDV--WNKCRFEWTDG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 IFVSFGLLVVFLS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37; Conservative
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                               26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66
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Matches
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A; Residues: 25-145, K',147-162 <MUR>
A;Note: 146-Arg was also found
C; Comment: This galactose-binding lectin is isolated from the coelomic fluid.
C;Comment: This protein plays important roles in defense mechanisms and in development C;Comment: The molecule is a tetramer of identical chains.
                                             The amino-acid sequence of a lectin of the acorn barnacle Megabalanus rosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 NDAQLACQTVHPGAYLATIQSQLENAFISETVSNNRLWIGLNDIDLEGHYVWSNGEATDF 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 NSSLKFC--ADKGSHLLITFPDNQGVNLFQEYVGEDFYWIGLRDID----GWRWEDGPALSL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 VMVALGLITVILMSLLLYQRTLCCGSKGFMCSQCSRCP-NL-WMRNGSHCYYFSMEKRDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- AITTGECT-CPGNLDWQEYDGHCYWASTYQVRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: tetranectin; C-type lectin homology C;Keywords: hemolymph; homotetramer; lectin F;1-24/Domain: signal sequence #status predicted <SIG>F;1-24/Domain: signal sequence #status predicted <SIG>F;25-162/Product: lectin BRA3-1 #status experimental <MAT>F;26-150/Domain: C-type lectin homology cLCH>F;26-150/Domain: C-type lectin homology secure experimental F;157/Disulfide bonds: interchain (to 160) #status experimental F;160/Disulfide bonds: interchain (to 157) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 10.8%; Score 112, DB 1; Best Local Similarity 26.4%; Pred. No. 0.0026; Matches 37; Conservative 17; Mismatches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: August 10, 2004, 16:44:40
Job time : 13.5 secs
                    Biophys. Acta 874, 285-295, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 SILS-----NSVVQKCGTIH 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 TYWSSNNPNNWENQDCGVVN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :: |: || |:
IVQAVTLLVVVF---
                                                                                                                                                                                                                                                                                                                                                                                         A; Introns: 22/1; 47/2; 86/3
                                                A; Title: The amino-acid se A; Reference number: A26094
                                                                                                                                                         A; Molecule type: protein
                                                                                                                   A; Accession: A26094
                                                                                                                                                                                                                                                                                                                                                         C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lectin BRA3-2 precursor - barnacle (Megabalanus rosa)
C;Species: Megabalanus rosa
C;Species: Megabalanus rosa
C;Accession: JC1504, A26094
R;Takamatsu, N.; Takeda, T.; Kojima, M.; Heishi, M.; Muramoto, K.; Kamiya, H.; Shiba, T. A;Tile: Acorn barnacle Megabalanus rosa lectin (BRA-3): cDNA cloning, gene structure an A;Reference number: JC1503; MJID:93292994; PMID:8514190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coelomic fluid.
and in development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-162 < TAK>
B; Muramoto, K.; Kamiya, H.
Biochim. Biophys: Acta 874, 285-295, 1986
A; Title: The amino-acid sequence of a lectin of the acorn barnacle Megabalanus rosa.
A; Reference number: A26094
                                                3;
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                                                                                                            --LLLYORTLCCGSKGFMCSQCSRCPNLWMRNGS 84
                                                                                                                                                                              --CKEGWVGYNK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80
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                                                                                                                                                                                                                                          HCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGLRDID 139
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: protein
A,Residues: 25-162 <MUR>
A,Residues: 25-162 <MUR>
A,Rote: 146-Arg was also found
C;Comment: This three galactose-binding lectin is isolated from the coel
C;Comment: This protein plays important roles in defense mechanisms and
C;Comment: The molecule is a tetramer of identical chains.
C;Comment: The molecule is a tetramer of identical chains.
C;Comment: The molecule is a tetramer of identical chains.
C;Comment: The molecule is a tetramer of identical chains.
C;Comment: The molecule is a tetramer of identical chains.
C;Comment: The molecule is a tetramer of identical chains.
C;Comment: The molecule is a tetramer of identical chains.
C;Comment: The molecule is a tetramer of identical chains.
C;Comment: The molecule is a tetramer of identical chain.
C;Comment: This protein interchain (to 160) #status experimental
F;160/Disulfide bonds: interchain (to 157) #status experimental
                                                28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 162;
                                             Indels
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      22.6%; Pred. No. 0.0015;
ive 20; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
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30.3%; Pred. No. 0.0023;
live 14; Mismatches 45
                                                                                                                                                                       PCGS--IIIVLSVFVIILSTRPPVPPDIKILY--
                                                                                                        PCVSYLVMVALGLLTVILMS-
Best Local Similarity 22.6
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A26094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: JC1504
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an

lectin BRA3-1 precursor - barnacle (Megabalanus rosa)
C;Species: Megabalanus rosa
C;Species: Megabalanus rosa
C;Date: 24-Feb-1994 #sequence_revision 09-Sep-1994 #text_change 16-Jul-1999
C;Accession: JCI503; Az6094
R;Takamatsu, N.; Takeda, T.; Kojima, M.; Heishi, M.; Muramoto, K.; Kamiya, H.; Shiba, Gene 128, 251-255, 1993
A;Title: Acorn barnacle Megabalanus rosa lectin (BRA-3): cDNA cloning, gene structure A;Reference number: JCI503; MUID:9329994; PMID:8514190

A;Accession: JCL503
A;Molecule type: DNA; mRNA
A;Residues: 1-162 <TAK>
A;Coss-references: DDBJ:113299
R;Muramoto, K.; Kamiya, H.

81

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126 VGEDFYWIGLRDID---GWRWEDGPALSLSILS-

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(otasu) Andia egod sint

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 10, 2004, 16:36:04; Search time 8 Seconds . :

(without alignments) 1223.649 Million cell updates/sec

1 MADNSIYSTLELPAAPRVQD......GLHASSCEVALQWICEKVLP 188 US-09-811-367B-5 1036 Perfect score: Sequence:

52070155 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 141681 seqs, Searched:

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 188

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		عد			SUMMARIES		
Result No.	Score	Query Match	Length	DB	ID	Description	
н	w		179	н	CD94 MACMU	O9mzk9 macaca mula	
N	155	15.0	179	Н	CD94 HUMAN	apie	
m	155	15.0	179	Н	CD94_PANTR	pan t	
4	154	14.9	163	Н	V239 FOWPV	P14371 fowlpox vir	
ស	153.5	14.8	149	Н	CLE2_HUMAN		
9	148.5	14.3	133	Ч	RHCA_AGKRH	P81397 agkistrodon	
7	140.5	13.6	148	Н	CVXB_CRODU		
æ	137	13.2	167	Н	VOOB FOWPV	0 fowlbox v	
σ	132.5	12.8	117	Н	CHBB_CROHO		
10	131	12.6	157	Т	MMHA AGKHA	agkistrod	
11	130	12.5	146	1	MMHB_AGKHA		
12	127.5	12.3	146	П	IXB TRIFL		
13	126	12.2	133	Н	BOTA BOTJA		
14	4	12.0	123	Н	ABA4_TRIAB		
15	123.5	11.9	125	Н	BOTB BOTJA		
16	113	10.9	162	Н	LEC3 MEGRO	9 megabalar	
17	111.5	ö	158	Н	CVXA_CRODU		
18	109.5	ö	125	Н	ABA3_TRIAB	_	
19	109.5	10.6	155	Н	PLC HALLA		
20	107.5	10.4	129	Н	RHCB AGKRH	~	
21	106.5	10.3	118	Н	ABBB_TRIAB		
22	103.5		131	Н	ABA1 TRIAB	_	
23	103.5		175	Н	PAP1_HUMAN	_	
24	103	9	174	Н	PAP3 MOUSE	mus m	
52	0		9	Н	LITA HUMAN	P05451 homo sapien	
26		•	133	П	ECHA_ECHCA	echis	
27	0	٠	3	П	LECG_CROAT	~	
28	99.5	•	3	٦	ABA2 TRIAB	~	
29	98		158	۲	NKGF PANTR		
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31	9	9.4	158	1		-	
32	96.5	9.3	123	П	m	echis	
33	96.5	•	152	Н	IXA TRIFL		

Q9psm4 lachesis st P48304 homo sapien P35230 mus musculu Q08731 mus musculu Q9psn0 bitis ariet Q9ygp1 trimeresuru P42854 rattus norv P17346 megabalanus P25031 rattus norv C09037 mus musculu P05140 hemitripter P81115 trimeresuru	
LECG LACST LITB_HUMAN PAP1 MOUSE LITZ_MOUSE LITZ_MOUSE LECG_BITAR LECG_TRIST PAP3 RAT PAP3 RAT PAP2 MOUSE ANP HEMAN ANP HEMAN ABBA TRIAB	
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135 175 173 173 173 173 173 175 1163	
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9 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	
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ALIGNMENTS

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch). Kravitz R.H., Grendell R.L., Slukvin I.I., Golos T.G.;
'Selective expression of NKG2-A and NKG2-C mRNAs and novel alternative
splicing of 5' exons in rhesus monkey decidua.";
Immunogenetics 53:69-73(2001). SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
MEDLINE=20322487; PubMed=10866118;
LaBonte M.L., Levy D.B., Letvin N.L.;
"Characterization of rhesus monkey CD94/NXG2 family members and identification of novel transmembrane-deleted forms of NKG2-A, B, C, and D."; -!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells.-!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family CD94_MACMU STANDARD; PRT; 179 AA.

Q9MXZ6; Q9GK91; Q9MXX7; Q9MXX8;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 42, Last sequence update)
10-COT-2003 (Rel. 42, Last annotate)
Natural killer cells antigen CD94 (NK cell receptor subfamily D, member 1). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Name=3; Synonyms=CD94 alt; IsoId=Q9MZK9-3; Sequence=VSP 003054; -!- TISSUE SPECIFICITY: Natural killer cells. -!- SIMILARITY: Contains 1 C-type lectin family domain. members.
-!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=3;
Name=1; Synonyms=CD94-A;
IsoId=Q9MZK9-1; Sequence=Displayed; Name=2; Synonyms=CD94-B; IsoId=Q9MZK9-2; Sequence=VSP_003055; SEQUENCE FROM N.A. (ISOFORM 1). MEDLINE=21158386; Pubmed=11261935; Immunogenetics 51:496-499(2000). Macaca mulatta (Rhesus macaque) Cercopithecinae, Macaca. NCBI_TaxID=9544; KLRD1 OR CD94. RESULT 1 CD94 MACMU

EMBL; AF190931; AAF74527.1; -. EMBL; AF190932; AAF74528.1; -.

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Biassoni
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4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGED 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDCCSCHEKWVGYRCNCYF1SSEEKTWNESRHFCASOKSSLLOLONRDELDFMSS--SQH 113
                                                                                                          TYPE LECTIN 1; FALSE_NEG.
TYPE_LECTIN 2; 1.
Glycoprotein; Transmembrane; Signal-anchor; Lectin;
                                                                                                                                                                                                                                                                                                                                                                      MAVFKTTLWRLISGTLGIICLSLMATLGILLKNS -> MAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FYWIGL ----RDIDGWRWEDGPALSLSILSNSVVQK---CGTIHRCG-LHASSCEVALQWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                   SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chang C., Rodriguez A., Carretero M., Lopez-Botet M., Phillips J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD94 HUMAN STANDARD; PRT; 179 AA. 01341; 043321; 043773; 09UBE3; 09UBQ0; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-WAR-2004 (Rel. 43, Last sequence update) 15-WAR-2004 (Rel. 43, Last annotation update) 16-WAR-2014 (Rel. 43, Last annotation update) 16-WAR-2014 (Rell 43, Last annotation update) 16-WAR-2014 (Rell 50) (Killer cell 16-Cin-like receptor subfamily D, member 1) (KP43). KIRD1 OR CD94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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MEDLINE=98139529; PubMed=9472066;
Rodriguez A., Carretero M., Glienke J., Bellon T., Ramirez A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lanier L.L.;
"Molecular characterization of human CD94: a type II membrane glycoprotein related to the C-type lectin superfamily.";
Eur. J. Immunol. 25:2433-2437(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.8%; Score 163.5; DB 1; Length 179; 31.2%; Pred. No. 4.7e-09; tive 19; Mismatches 58; Indels 9;
                                                                                                                                                                                                                                                       C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06212B4494527F07 CRC64;
                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                         (in isoform 3).
/FTId=VSP 003054.
L -> LQ (in isoform 2).
/FTId=VSP 003055.
                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                        (POTENTIAL).
                                                                                                                                                                    Polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96011848; PubMed=7589107;
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                                                    InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
               EMBL; AF294886; AAG34498.1; -.
HSSP; P22897; 1EGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20607 MW;
EMBL; AF190933; AAF74529.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 31.29
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                105
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132
34
                                                                                                          PROSITE; PS00615; C_TY
PROSITE; PS50041; C_TY
Antigen; Receptor; Gly
Alternative splicing;
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179 AA;
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DISULFID
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CARBOHYD
VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22388257; PubMed=12477932;

A REDLINE=22388257; PubMed=12477932;

A Lausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buttow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buttow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Altschul S.F., Zeeberg B. Bonaldo M.F., Casavant T.L., Scheefz T.E.,

B Latchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheefz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., L.J.,

Raden J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tadokoro K.,
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-!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
-!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98267245; PubMed=9601951;
Furnkawa H., Yabe T., Watanabe K., Miyamoto R., Akaza T.,
Tohma S., Inoue T., Yamamoto K., Juji T.;
"A alternatively spliced form of the human CD94 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=1; Synonyms=CD94-A; Isoquence=Displayed; Name=2; Synonyms=CD94-B; Isoquence=VSP_003053; Isod=Q13241-2; Sequence=VSP_003053; Isod=Q13241-2; Sequence=VSP_003052; Isod=Q13241-3; Sequence=VSP_003052; -:- TISUB SPECTRICITY: Natural kiler cells.
-:- SIMILARITY: Contains 1 C-type lectin family domain.
-:- DATABASE: NAME=PROW; NOTE=CD guide CD94 entry; WWW="http://www.ncbi.nlm.nlh.gov/prow/cd/cd94.htm".
                                                                                                                                                                                                                                                                                     Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
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--- SUBCELLUIAR LOCATION: Type II membrane protein.
--- ALTERNATIVE PRODUCTS:
Lebrach H., Francis F., Lopez-Botet M.;
"Structure of the human CD94 C-Type lectin gene.";
Immunogenetics 47:305-309(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y14287; CAA74663.1; -.
Y14288; CAA74663.1; JOINED.
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RESULT 4
V239 FOWPV
ID V239 FOWPV STANDARD;
AC P14371; Q9J500;
DT 01-JAN-1990 (Rel. 13, Created)
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                                    genes.";
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                RGO; GO:0005886; C:plasma membrane; TAS.
RGO; GO:0004888; F:transmembrane receptor activity; TAS.
RGO; GO:0004888; F:transmembrane receptor activity; TAS.
RGO; GO:0004686; F:antimicrobial humoral response (sensu Inver. .; TAS.)
RGO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
RF Ffam; PF00059; lectin_C: 1.
RFAMRT; SM00034; CLECT; 1.
RFAMRT; SM00034; CLECT; 1.
RFAMRT; SM00015; C_TYPE_LECTIN_1; FALSE_NEG.
RFAMF; PS000615; C_TYPE_LECTIN_2: 1.
RAIGEM: RECEPTOR; GlyCoprotein; Transmembrane; Signal-anchor; Lectin;
MALTERALSMEM 1 3 STRUCTURE.
CYTOPLASMIC (POTENTIAL).
RFAMNSMEM 1 3 STRUCTURE.
RFAMNSMEM 1 3 SPONDATIAL).
RFAMNSMEM 1 1 STRUCTURE.
RFAMNSMEM 1 1 1 REPRESENTED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 GYRCNCYFISSEQKTWNESRHLCASQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEE 124
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MAVFKTTLWRLISGTLGIICLSLMATLGILLKNS -> MAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 IDGWRWEDGPALSLSILSNSV---VQKCGTIHRCG-LHASSCEVALQWICEKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20350666; PubMed=10894168;
Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L.,
Muir D.G., Canavez F., Cooper S.L., Valiante N.M., Lanier L.L.,
                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Killer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Rapid evolution of NK cell receptor systems demonstrated by comparison of chimpanzees and humans."; Immunity 12:687-698 (2000).
                                                                                                                                                                                                                                                                                                                                                15.0%; Score 155; DB 1; Length 179; 27.0%; Pred. No. 3.2e-08;
                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                           1884D99E8D9583A7 CRC64;
                                                                                                                                                                                             C-TYPE LECTIN (LONG FORM)
BY SIMILARITY.
                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Natural killer cells antigen CD94 (NK cell receptor)
lectin-like receptor subfamily D, member 1).
KIRD1 OR CD94.
                                                                                                                                                                                                                                                                                         P_003052.
(in isoform 2).
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/FTId=VSP 003053.
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                                                                                                                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                           20497 MW;
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HGNC: 6378; KLRD1
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176
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174
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                                                                                                                                                                                                                                                                                                                           179 AA;
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Matches 47; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80
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InterPro: IRR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SWART; SM00034; CLECT; 1.
PROSITE; PS00614; C_TYPE_IECTIN_1; FALSE_NEG.
PROSITE; PS00614; C_TYPE_LECTIN_2; 1.
Antigen; Receptor; G_Type_Lectin; Transmembrane; Signal-anchor; Lectin; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 WK-VKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTLCCGSKGFM--CSQCSRCPNLWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 WRLISGTLGIICLS -- LMATLGILLKNSFTKLSIEPAFTPGPNIELQKDSDCCSCQEKWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 RNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGL---RD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Gaps
                                                                                                                                                  -!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells. -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I., Cleland S., Guethlein L.A., Uhrberg M., Parham P., "Conservation and variation in human and common chimpanzee CD94 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 IDGWRWEDGPALSLSILSNSVV---QKCGTIHRCG-LHASSCEVALQWICEKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 HTAWLWENGSALSQYLFPSFETFNPKNCIAYNPNGNALDESCEDKNRYICKOOL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q9MZ41-1; Sequence=Displayed;
Name=2; Synonyms=CD94-B;
IsoId=Q9MZ41-2; Sequence=VSP 003056;
-!- TISSUB SPECIFICITY: Natural killer cells.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7244D99E8D9587E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L -> LQ (in isoform 2).
/FTId=VSP_003056.
                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist:
                                                                                                                                                                                                                                                                                                                                                                                isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.0%; Score 155; DB 1; 27.0%; Pred. No. 3.2e-08; cive 28; Mismatches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (sor send an email to license@isb-sib.ch)
                                                                                                                           Immunol. 168:240-252(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF259054; AAF86964.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                          Name=1; Synonyms=CD94-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 27.0°
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179
176
72
174
174
166
166
105
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31
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163 AA.

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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                  complex.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swigs Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 NCYFFSEEKNNKSLAVERCKDMDGHLTSISSKEEFKFILRYKGPGNHWIGIEKVDFNGTW 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLE2_HUMAN STANDARD; PRT; 149 AA.
092478; 098878; 098084;
28-FEB-2003 (Rel. 41, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
C-type lectin superfamily member 2 (Activation-induced C-type lectin).
CLECSF2 OR ALCL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCVSYLVMVALGLITVILMS-----LLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tomley F., Binns M., Campbell J., Boursnell M.E.G.;
"Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                 Fowlpox virus (FPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                           MEDLINE=20193820; PubMed=10729156;
Afonso C.L., Tulhan B.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
"The genome of fowlpox virus.";
J. Virol. 74:3815-3831(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : ||| : :|| : :|| : || : || :| | : || :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 RWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQWICEKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of fowlpox virus.";
J. Gen. Virol. 69:1025-1040(1988).
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 AA; 18635 MW; 5156DC8928855532 CRC64;
      16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative C-type lectin protein FPV239 (BamHI-ORF8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.9%; Score 154; DB 1; 22.9%; Pred. No. 3.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PERMY PRO01334; Lectin C.
Pfam; PR00059; lectin c; 1.
SMART; SM0004; CLECT; 1.
PR005TE; P800615; C TYPE LECTIN 1; PALSE NEG.
PROSITE; P850041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 PCGS--IIIVLSVFVIILSTRPPVPPDIKILY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C-TYPE LECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=88229622; PubMed=2836548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF198100; AAF44583.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=FP-9 / Isolate HP-438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, D00295, BAA00203.1, -. PIR, H29963, WMVZF8.
HSSP, P05140, 2AFP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-116 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A.
                                                                                                                                                                                                                                  NCBL_TaxID=10261;
                                                                                                                                                                                                       Avipoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
             d
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TISSUBLINE FROM N.A.

TISSUB-CTINATY bladder;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brossk S.A., McEwan P.J., McKernan R.J., Malke J.A., Gunarane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Marra M.A.;

"Manner D.M. A., Schein J.E., Jones E. Warra M.A.;

"Manner D.M. A., Schein J.E., Jones E. Warra M.A.;

"Manner D.M. A., Schein J.E., Jones E. Warra M.A.;

"Manner D.M. A., Schein J.E., Jones E. Warra M.A.;

"Manner D.M. A., Schein J.E., Jones E. W.,

"Manner D.M. A., Schein J.E., Jones E. W.,

"Manner D.M. A., Schein J.E., Jones E. W.,

"Manner D.M. A., Schein J.E., Jones E. W.,

"Manner D.M. A., Schein J.E., Jones E. W.,

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"Manner D.M. A., Schein J.E., Jones E. W.,

"Manner D.M. A., Schein J.E., Jones E. W.,

"Manner D.M. A., Schein J.E., Jones E. W.,

"Manner D.M. A., Schein J.E., Jo
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GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005530; F:Lectin; TAS.
GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . .; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINES-99173880; PubMed=10072769;
Yokoyama-Kobayashi M., Yamaguchi T., Sekine S., Kato S.;
Yokoyama-Kobayashi M., Yamaguchi T., Sekine S., Kato S.;
"Selection of cDNAs encoding putative type II membrane proteins on the cell surface from a human full-length cDNA bank.";
Gene 228:161-167(1999).
                                                                                                                                                                                               Hamann J., Montgomery K.T., Lau S., Kucherlapati R., van Lier R.A.W., "ALCL, a new activation induced antigen encoded by the human NK gene
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-!- SUBCELIULAR LOCATION: Type II membrane protein (Probable).
-!- TISSUE SPECIFICITY: Expressed preferentially in lymphoid tissues, and in most hematopoletic cell types.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
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EXTRACELLULAR (POTENTIAL)
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BY SIMILARITY.
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                                                                                                     SEQUENCE FROM N.A. MEDLINE=97190245; PubMed=9038101;
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Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                               49
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"Rhodocetin, a novel platelet aggregation inhibitor from the venom of calloselasma rhodoseroma (Malayan pit viper): synergistic and noncovalent interaction between its subunits.";

Biochemistry 38:7584-7593(1999).

- FUNCTION: A potent inhibitor of collagen-induced platelet aggregation. Individually, neither subunit inhibits platelet aggregation. Both subunits are essential.

- SUBUNIT: Heterodimer of one alpha and one beta subunit held
                                                                                                                                                                                                                                                                  31 HRPCVSYL-VMVALGLLTVILMSLLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- MASS SPECTROMETRY: MW=15955.90; MW ERR=1.44; METHOD=Electrospray.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
HSSP; P23806; 1IXX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma)
Bukaryota, Matazoa; Chordate; Craniata; Vertebrata; Buteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Calloselasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       together by noncovalent interactions rather than by intersubunit
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                                        (POTENTIAL).
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                                                                           .) (POTENTIAL)
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                                                                                                                                                                   14.8%; Score 153.5; DB 1; Length 149; 27.0%; Pred. No. 3.7e-08;
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386EAC519DFC674D CRC64;
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE, FUNCTION, SUBUNIT, AND MASS SPECTROMETRY.
                                                                                                                                                                                                        68;
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                                                                         N-LINKED (GLCNAC.
M -> T (IN REF. 3)
D -> H (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
18-FBB-2003 (Rel. 41, Last annotation update)
Rhodocetin alpha subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00059; lectin c; 1.
SMART; SM0034; CLECT; 1.
PROSITE; PS00615; C TYPE_LECTIN 1; FALSE_NEG-PROSITE; PS05041; C TYPE_LECTIN 2; 1.
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27; Mismatches
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133 AA;
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Best Local Similarity
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NCBI_TaxID=8717;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                              61 NKIYRSWIGLKIENKGORSNLEWSDGSSISYENLYEPYMEKCFLMDHOSGLPKWHTADCE 120
CPNLWMRNGSHCYYFSMEKRDWNSSLKFCA--DKGSHLLTFPDNQGVNLFQEYVGEDFY- 131
                             2 CPDGWSSIXSYCYRPFKEKKIWEEAERFCTEQEKEAHLVSM-ENRLEAVFVDMVMENNFE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C-TYPE LECTIN.
INTERCHAIN (WITH C-158 IN ALPHA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERCHAIN (WITH C-104 IN ALPHA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Crotalus durissus terrificus (South American rattlesnake).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leduc M., Bon C.;
"Cloning of subunits of convulxin, a collagen-like platelet-
"Cloning of subunits of corvalus durissus terrificus venom.";
Biochem. J. 333:389-333(1998).
-!- FUNCTION: Binds to the platelet and collagen receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 24-53; 99-109 AND 126-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 140.5; DB 1; Length 148; Pred. No. 7.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 1 C-type lectin family domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONVULXIN BETA.
                                                                                                                                                                                                                                                                                                                                                                                        148 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00615; C_TYPE_LECTIN_1; 1. PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Convulxin beta precursor (CVX beta).
                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Venom gland;
MEDLINE=98324901; PubMed=9657980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viperidae; Crotalinae; Crotalus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam, PF00059, lectin c; 1.
PRINTS, PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MM;
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29.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Y16349; CAA76182.1; -.
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SIGNAL
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17402 I
                                                                                                                                                                                                      177 VALQWICEKVLP 188
                                                                                                                                                                                                                                                       121 EKNVFMCKFQLP 132
                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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144
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148 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8732;
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26
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Matches
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                                                                                                                RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
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                                        39 VMVALGLLTVILMSLLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNS 98
                                                                                                                                   SLKFCADK--GSHLLTFPDNQGVN----LFQEYVGEDFYWIGLRDI---DGWRWEDG 146
                                                                                                                                                                51 AEKFCTQQHTGSHLVSFHSTEEVDFVVKMTHQSLKSTFFWIGANNIMNKCNWQWSDG 107
                                                                       MEDLINE=88229622; PubMed=2836548;
Tomley F., Binns M., Campbell J., Boursnell M.E.G.;
"Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | : | | : | : | | : | | : | | : | | VSCYAITVLGILCLILFTILV---VVTCKWYYAFPYFSKVCPDEWIGYNSKCYYFTINET
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  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fowlpox virus (FPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20193820; PubMed=10729156;
Afonso C.L., Tulman B.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
"The genome of fowlpox virus.";
  23;
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                                                                                                                                                                                                                                                                                                                                                   01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative C-type lectin protein FPV008/FPV253 (BamHI-ORF2).
FPV008 AND FPV253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.2%; Score 137; DB 1; Length 16'
29.1%; Pred. No. 1.8e-06;
.ive 21; Mismatches 78; Indels
39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . Virol. 74:3815-3831(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C769ECAA8AD238ED CRC64;
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SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; FALSE NEG.
PROSITE; PS50041; C TYPE LECTIN 2; 1.
                                                                                                                                                                                                                                                                                                 167 AA.
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C-TYPE LECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gen. Virol. 69:1025-1040(1988).
21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D00295; BAA00192.1; -.
EMBL; AF198100; AAF44607.1; -.
EMBL; AF198100; AAF44608.1; -.
                                                                                                                                                                                                                                                                                                                                            (Rel. 13, Created)
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InterPro, IPR001304; Lectin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 AA; 19869 MW;
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les 44; Conservative
Conservative
                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fowlpox virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10261;
                                                                                                                                                                                                                                                                                                                                          01-JAN-1990
                                                                                                                                                                                                                                                                                          V008 FOWPV
P14370;
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Matches
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Matches
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75 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADK--GSHLLITFPDNQGVNLFQEYVGEDFYW 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERCHAIN (WITH C-81 IN ALPHA CHAIN) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Mamushigin alpha chain precursor.
Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                          Crotalus horridus horridus (Timber rattlesnake).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostc Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Crotalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 117;
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                                                                                                                                                (Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
 185
                              124 EQGVNDICLLFDTSNIIEMSCIFHERTICVK 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C-TYPE LECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY
BY SIMILARITY
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155 SNSVVQKCGTIHRCGLHASSCEVALQWICEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                       IISSUE=Venom;
MEDLINE=96420502; PubMed=8823201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 IGLRDIDGW-----RWEDG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | | | | : | | | | MGWRDI--WNERRLQWSDG 78
                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00059; lectin_c; 1. TerinTrans; PR00356; ANTIFREEZEII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13888 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116
13
115
92
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                                                                                                                                                                                CHH-B beta subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9229
                                                                                                                                                     28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MMHA AGKHA
Q9YGG9;
                                                                                                         CROHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                         CHBB CR
P81509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGKHA
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98319530; PubMed=9657448; Sakurai Y., Fujimura Y., Kokubo T., Imamura K., Kawasaki T., Handa M., Suzuki M., Matsui T., Titani K., Yoshioka A.; "The cDNA cloning and molecular characterization of a snake venom platelet glycoprotein Ib-binding protein, mamushigin, from Agkistrodon halys bromhoffii venom."; Thromb. Haemost. 79:1199-1207(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: Binds to platelet glycoprotein Ib and enhances platelet aggregation at low-shear stress. At high-shear stress, aggregation
                                                                                                                                                                                                                                          SEQUENCE FROM N.A., SEQUENCE OF 24-56, SUBUNIT, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 VMVALGLITVILMSLLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 IFLSFGLLVVFVS------LSGTGADCPSDWSSYEGHCYRVFQKEMTWED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 SLKRCAD--KGSHLLTFPDNQG----VNLFQEYVGEDFYWIGLRDIDGW-----RWEDGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERCHAIN (WITH C-103 IN ALPHA CHAIN)
                    10-0CT_2003 (Rel. 42, Created)
10-0CT_2003 (Rel. 42, Last sequence update)
10-0CT_2003 (Rel. 42, Last annotation update)
Mamushigin beta chain precursor.
Mamushigin beta chain precursor.
Manushigin beta chain precursor.

Manushigin beta chain precursor.

Manushigin beta chain precursor.

Manushigin beta chain precursor.

Manushigin beta chain precursor.

Euchidosauria, Squamata; Scleroglossa, Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Secreted.
-!- MASS SPECTROMETRY: MW=15413; MW_ERR=6; METHOD=Electrospray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Heterodimer of alpha and beta chains; disulfide-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9EDA84BDCC24E76D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 ALSLSILSNSVVQKCGTIHRCGLHASSCEVAL----QWI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.5%; Score 130; DB 1; 24.5%; Pred. No. 7.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAMUSHIGIN BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY)
BY SIMILARITY.
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BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE, PS00615; C TYPE LECTIN 1; 1. PROSITE; PS50041; C TYPE LECTIN 2; 1. Blood coagulation; Lectin; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005576; C:extracellular; IC. GO; GO:0007596; P:blood coagulation;
                                                                                                                                                                       Viperidae; Crotalinae; Gloydius NCBI_TaxID=242054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001304; Lectin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB019616; BAA34425.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00059; lectin c; 1. SMART; SM00034; CLECT; 1.
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146
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Matches 39; Conserv
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 SLKFCADK--GSHLLTFPDNQGVNLFQEYVGE-----DFYWIGL-----RDIDGWRWEDG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----SGAE----DDSDCPSDWSSNGRFCYKLFQQKMKWAD 50
                                                                                                 TISSUE-Venom;
MEDLINE-98319530; PubMed=9657448;
MEDLINE-98319530; PubMed=9657448;
Sakurai Y., Fujimura Y., Kokubo T., Imamura K., Kawasaki T., Handa M., Suzuki M., Matsui T., Titani K., Yoshioka A.;
"The CDNA cloning and molecular characterization of a snake venom platelet glycoprotein Ib-binding protein, mamushigin, from Agkistrodon halys bromhoffii venom.",
Thromb. Haemost. 79:1199-1207(1998).
-- FONCTION: Binds to platelet glycoprotein Ib and enhances platelet aggregation at low-shear stress. At high-shear stress, aggregation is inhibited.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 VMVALGLLIVILMSLLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNS
                                                                              SEQUENCE FROM N.A., SEQUENCE OF 22-58, SUBUNIT, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C-98 IN BETA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Secreted.
MASS SPECTROMETRY: MW-16825; MW_ERR=2.7; METHOD=Electrospray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
  Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                           SUBUNIT: Heterodimer of alpha and beta chains; disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52; Indels
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BY SIMILARITY.
47DAA17891CE1865 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Contains 1 C-type lectin family domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAMUSHIGIN ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 131; DB 1;
Pred. No. 6.5e-06;
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BY SIMILARITY.
BY SIMILARITY.
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GO; GO:0007596; P:blood coagulation; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; 1.
PROSITE; PS50041; C TYPE_LECTIN_2; 1.
Blood coagulation; Dectin; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis ac.
Lepidosauria; Squamata; Sclerog
Viperidae; Crotalinae; Gloydius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00059; lectin c; 1.
PRINTS; PR01504; PNCREATITSAP.
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HSSP; P23806; 1IXX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 PALSISISNSVVOKC 162
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27.2%;
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152
152
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151
103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                 NCBI_TaxID=242054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22
34
27
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103
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MMHB_AGKHA
ID MMHB_AGKHA
                                                                                                                                                                                                                                                                                                                                                                    linked
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DISULFID
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7;

48; Gaps

--HNAWITESECIAAKTTDNOWL 130

107 RLS---

146 AA.

PRT;

STANDARD;

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Length 146; 52; Indels us-09-811-367b-5.closed.rsp

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146 AA;
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TISSUE=Venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1991
01-JUL-1993
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                  DISULFID
                                       DISULFID
                                                         TURN
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STRAND
HELIX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                      Matsuzaki R., Yoshihara B., Yamada M., Shima K., Atoda H., Morita T., "cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant protein from snake venom.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97331317; PubMed=9187649; Mizuno H., Fujimoto Z., Koizumi M., Kano H., Atoda H., Morita T.; Mizucture of coagulation factors IX/X-binding protein, a heterodimer of C-type lectin domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nat. Struct. Biol. 4:438-441 (1997).

-!- FUNCTION: Anticoagulant protein which binds with factor IX and factor X in the presence of calcium with a 1 to 1 stoichiometry.
-!- SUBUNIT: Heterodimer of Chains A and B; disulfide-linked.
-!- SUBCELLULAR LOCATION: Secreted.
-!- MISCELLANBOUS: Calcium is required for ligand binding.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COAGULATION FACTOR IX/FACTOR X-BINDING PROTEIN B CHAIN.
C-TYDE LECTIN (LONG FORM).
BY SIMILARITY.
                                                                                                                                                                                                   Trimeresurus flavoviridis (Habu).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Atoda H., Hyuga M., Morita T.; "The primary structure of coagulation factor IX/factor X-binding protein isolated from the venom of Trimeresurus flavoviridis.
                                                                                                                                                                             Coagulation factor IX/factor X-binding protein B chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homology with asialoglycoprotein receptors, proteoglycan core protein, tetranectin, and lymphocyte Fc epsilon receptor for immunoglobulin B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. Biophys. Res. Commun. 220:382-387(1996)
                                                                                                                 (Rel. 20, Created)
(Rel. 36, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00034; CLECT; 1.
PROSITE; PS00615; CTYPE_LECTIN_1; 1.
PS051TE; PS550041; CTYPE_LECTIN_2; 1.
Lectin; Calcium; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 266:14903-14911(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDB; 1IXX; 06-MAY-98.

PDB; 1BJ3; 16-AUG-99.

INTERPRO; IPR001304; Lectin C.

INTERPRO; IPR003909; Pancreātis_ac.

PÉRM; PF00059; lectin c; 1.

PRINTS; PR01504; PNCRĒATITSAP.
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=96184662; PubMed=8645314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91332000; PubMed=1831197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D83332; BAA11888.1; -. PIR; JC4691; JC4691.
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36
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                                                                              IXB_TRIFL
P23807; Q91247;
01-NOV-1991 (Re]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Venom;
                                                                                                                                        15-JUL-1998
                                                                                                                                                          10-OCT-2003
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DISULFID
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                                           RESULT 12
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99 SLKFCADK--GSHLLTFPDNQGVNL----FQEYVGEDFYWIGLRDI---DGWRWEDGPA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 VMVALGLLTVILMSLLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNS 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --LSGTAADCPSDWSSYEGHCYKPFSEPKNWAD 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fulimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T., Fukui H., Sugimoto M., Ruggeri Z.M.;
"Isolation and chemical characterization of two structurally and functionally distinct forms of botrocetin, the platelet coagglutinin Biochemistry 30:1957-1964(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDILINE-93157385; PubMed-8430107; Usami Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui H., Titani K.; "Primary Structure of two-chain botrocetin, a von Willebrand factor modulator purified from the venom of Bothrops jararaca."; Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bothrops jararaca (Jararaca).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
                INTERCHAIN (WITH C-102 IN A CHAIN) BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 LRYKAWAEESYCVYFKSTNNK------WRSRACRMMAQFVCE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L-----SLSILSNSVVQKCGTIHRCGLHASSCEVALQWICE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16922 MW; 8E1961C59F96757C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1991 (Rel. 19, Created)
01-UUL-1993 (Rel. 26, Last sequence update)
10-CCT-2003 (Rel. 42, Last amnotation update)
Botrocetin, alpha chain (Platelet coagglutinin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.3%; Score 127.5; DB 1
20.7%; Pred. No. 1.3e-05;
iive 28; Mismatches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 AA
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Venom;
MEDLINE=91129280; PubMed=1993206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viperidae, Crotalinae, Bothrops.
NCBI TaxID=8724;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 20.75
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 IFMSFGFLVVFLS-
  142
134
134
134
134
144
147
110
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110
1113
1133
1133
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us-09-811-367b-5.closed.rsp

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BOTB BOTJA
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                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                         DISULPID
                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                 Lectin.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P22030;
                                                                                                                                                                                                                                                                                                                                                                                                                                               BOTB_BOTJA
                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  toxin botrocetin.";

Structure 10:943-550(2002).

- FUNCTION: Two-chain botrocetin forms an activated complex with rwo-chain botrocetin forms of platelet gglutination.

- FUNCTION: There are two distinct forms of the von Willebrand factor-dependent platelet coagglutinin. The dimeric form is 34-times more active than the one-chain botrocetin in promoting vWF binding to platelets.

- SUBDINIT: Disulfide-linked dimer of an alpha and a beta chain.

Botrocetin and vWF form a soluble complex.

- SUBCELIULAR LOCATION: Secreted.

- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      platelets.";
Thromb. Haemost. 79:609-613(1998).
-!- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
agglutination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCAD--KGSHLLTFPDNQGVNLF---QEYVGE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                            "Structural basis of von Willebrand factor activation by the snake
                                                                                                                                                                                                                                                                                                                                                                                                                             INTERCHAIN (WITH C-75 IN BETA CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --DFY-WIGLRDID-----GWRWEDGPALSLSILSNSVVQKCGTIHR 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 VTKNIQSSDLYAWIGLRVENKEKQCSSEWSDGSSVSYENVVERTVKKCFALEK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alboaggregin A subunit 4.
Trimeresurus albolabris (White-lipped pit viper).
Rekaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
         X-RAY CRYSTALLOGRAPHY (2.6 ARGESTACE)
MEDLINE=22118144; PubMed=12121649;
Fukuda K., Doggett T.A., Bankston L.A., Cruz M.A., Diacovo T.G.,
Liddington R.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
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Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
Calvete J.J., Niewiarowski S.;
"Alboaggregins A and B. Structure and interaction with human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       15215 MW; E4CF4502946AC74B CRC64;
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; Pred. No. 1.7e-05;
24; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.2%; Score 126;
                                                                                                                                                                                                                                                PIR; A47267; A47267.
PDB; 11JK; 17-JUL-02.
PDB; 1FWU; 14-FRB-01.
InterPro; 1PR002353; AntifreezeII.
InterPro; 1PR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
PRINTS; PR00356; ANTIFREEZEII.
                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00615; C TYPE LECTIN 1; PROSITE; PS50041; C TYPE LECTIN 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                               128
80
                                                                                                                                                                                                                                                                                                                                              SM00034; CLECT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 30; Conserv
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P81114;
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셤
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75 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCAD--KGSHLLTFPDNQG----VNLFQEYVGE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CPSDWSSYEGHCYRVFNEPQNWADAEKFCTQQHKGSHLVSFQSSEEADFVVQMTRPIINA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fujimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T., Fukui H., Sugimoto M., Ruggeri Z.M.;
"Isolation and chemical characterization of two structurally and thuctionally distinct forms of botrocetin, the platelet coagglutinin isolated from the venom of Bothrops jararaca.";
Biochemistry 30:1957-1964(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Primary structure of two-chain botrocetin, a von Willebrand factor modulator purified from the venom of Bothrops jararaca.";
Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Structure 10:943-950(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bothrops jararaca (Jararaca).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Usami Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fukuda K., Doggett T.A., Bankston L.A., Cruz M.A., Diacovo T.G.,
Liddington R.C.;
                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 123;
                                                                                                                                                                                                                                                                                                                                                                                      Indels
   2, 3 and
                                                                                                                                                                                                                                  C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W, D4CFBEE1219C9B1E CRC64;
                              -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                            12.0%; Score 124.5; DB 1;
31.4%; Pred. No. 2.2e-05;
tive 15; Mismatches 31;
SUBUNIT: Heterotetramer of the subunits 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1991 (Rel. 19, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Botrocetin, beta chain (Platelet coagglutinin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 DFYWIGLRDIDGW----RWEDGPAL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
MEDLINE=22118144; PubMed=12121649;
                                                                                                                     Pfam; PF00059; lectin c; 1.
PRINTS; PR00356; ANTIFREEZEII.
SMART; SM00034; CIECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; 1.
PROSITE; PS50041; C_TYPE_LECTIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLVWIGLSNL--WNQCNSQWSDGTXL
                                                                HSSP, P23807; IIXX.
InterPro; IPR002353; Antifreezell.
InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93157385; PubMed=8430107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91129280; PubMed=1993206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viperidae, Crotalinae, Bothrops.
                                                                                                                                                                                                                                                                                             111
14365 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE, AND DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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13
119
                    disulfide-linked.
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96
123 AA;
                                                                                                                                                                                                                                                                                                                                                               Similarity
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Local S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 CPPDWSSYEGHCYRFFKEWMHWDDAEFFCTEQQTGAHLVSFQSKEEADFVRSLTSEMLKG 61
                             pure control of the Complex Control of the von Wilebrand factor dependent platelet coagglutination.

-!- FUNCTION: There are two distinct forms of the von Wilebrand factor dependent platelet coagglutinin. The dimeric form is 34-times more active than the one-chain botrocetin in promoting vWP binding to platelets.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
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VWF, and the complex then binds to platelet GPIb, resulting in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 31.3%; Pred. No. 2.8e-05;
Matches 26; Conservative 12; Mismatches 32; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 AA; 15037 MW; 1ED2027ED817FCA0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 DVVWIGLSDV--WNKCRFEWTDG 82
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113
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DISULFID
DISULFID
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Search completed: August 10, 2004, 16:42:48 Job time : 9 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using sw model OM protein - protein search, August 10, 2004, 16:39:05; Search time 32 Seconds (without alignments) 1853.669 Million cell updates/sec Run on:

US-09-811-367B-5

1036 1 MADNSIYSTLELPAAPRVQD......GLHASSCEVALQWICEKVLP 188 Perfect score: Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

1017041 seqs, 315518202 residues Searched:

Total number of hits satisfying chosen parameters:

396094

Minimum DB seq length: 0 Maximum DB seq length: 188

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_archea:*
sp_bacteria:*
sp_fungi:* SPTREMBL 25:* Database

sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
sp_phage:*
sp_plant:*
sp_plant:*
sp_rodent:* sp_vertebrate:*
sp_unclassified:* sp_bacteriap:* sp_archeap:* rvirus:* 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

09g1f4 sus scrofa 08b124 mus musculu 0951g4 bos taurus 09g1f3 sus scrofa 09mhy8 pongo pygma 08wup7 homo sapien 054708 mus musculu 054707 mus musculu Q9r007 mus musculu Q64335 rattus norv O88713 mus musculu 088713 mus musculu Q9nzs1 homo sapien Description Q64335 O88713 Q9NZS1 O54708 O54707 Q9R007 Q8BL24 Q95JG4 Q9GLF4 П 1111911 Query Match Length DB 181 173 165 165 164 161 1185 1173 173 100.0 80.9 166.9 1166.9 1166.0 116 178 175 175 173 171 Score Result Ņ.

Q8spx0 sus scrofa Q9ny25 homo sapien Q8mji3 pongo pygma O35778 rattus norv

Q9NY25 Q8MJI3 Q35778

Q8SPX0

Q9GLF3 Q8MHY8 Q8WUP7

161.5 160 160

165

159.5 158.5 158.5

Ognzj6 macaca mula Ogr4k5 rattus norv Q9d18s rat cytomeg Q8mhy9 pongo pygma Q9ukg0 homo sapien Q9ukg0 homo sapien Q8mj4 pongo pygma Q8mj4 pongo pygma Q8mj4 pongo pygma Q8mj4 pomgo pygma Q8mj4 pomgo sapien Q9id37 homo sapien Q9iw1 agkistrodon Q9iw1 agkistrodon Q9iw1 agkistrodon Q9iw1 agkistrodon Q9iw1 agkistrodon Q9iw1 agkistrodon Q9iw1 agkistrodon Q8av98 trimeresuru Q80j86 mus musculu Q80z37 mus musculu Q90x9 mus musculu Q90x9 mus musculu Q90x9 mus musculu Q90x9 mus musculu Q90x9 mus musculu Q90x9 mus musculu Q90x9 mus musculu Q90x9 mus musculu Q90x9 mus musculu Q90x9 mus musculu Q90x9 mus musculu Q90x9 mus musculu Q90x9 mus musculu Q90x9 mus musculu Q90x9 muscaca mula Q90x9 muscaca mula	QBayas agkistrodon Q91841 agkistrodon Q71045 vipera lebe Q61972 mus musculu Q8mjh4 pongo pygma Q9ep94 mus musculu
Q9MZJ6 Q9R4K5 Q8R4K5 Q8RHX9 Q9DLSB Q9DLSB Q9DLXQ0 Q9UKQ0 Q9UKQ0 Q9UKP2 Q9HD37 Q9HD37 Q9HD37 Q9ED37 Q9ED37 Q9ED37 Q9EC36 Q9CS7 Q9EC36 Q9CS7 Q9EC36 Q9CS7	3 Q8AYA5 3 Q91841 3 Q7T045 1 Q61972 Q8MJH4 1 Q9EP94
185 6 1132 11132 11132 11132 11132 11132 11132 11132 11132 11146 1133 1133 1133 1133 1133 1133 113	158 136 146 1182 1162 1164 1164
######################################	133.1 122.9 12.8
158 157.5 157.5 157.5 157.5 157.5 157.5 144 144 144 144 144 144 144 144 144 14	135.5 134.5 134.5 134 132.5
7 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4 4 4 4 4 4 0 4 5 6 7 6 7 6 7 6 7 6 7 6 7 6 7 6 7 6 7 6

ALIGNMENTS

W SEQUENCE FROM N.A.

WEDLINE=96016176; PubMed=7568140;

A Guthmann M.D., Tall M., Pecht I.;

A Guthmann M.D., Tall M., Pecht I.;

A secretion inhibitory signal transduction molecule on mast cells is

RT another C-type lectin.";

RT another C-type lectin.";

BR EMBL, X97191; CAA55829.1; JOINED.

DR EMBL, X97192; CAA55829.1; JOINED.

DR EMBL, X97194; CAA55829.1; JOINED.

DR EMBL, X97195; CAA55829.1; JOINED.

DR EMBL, X97195; CAA55829.1; JOINED.

DR EMBL, X97195; CAA55208.1; JOINED.

DR EMBL, X97195; CAA55208.1; JOINED.

DR EMBL, X97195; CAA55208.1; JOINED.

DR EMBL, X97195; CAA55208.1; JOINED.

DR FMAL, S970034; CAECT, Rattus norvegicus (Rat). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. SEQUENCE FROM N.A.
STRAIM=SPRAGUE DAWLEY; TISSUE=Testis;
BOCEK Jr. P. Guthmann M.D., Pecht I.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases. Last sequence update) Last annotation update) 188 AA. Created) PRT; Q64335; 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-OCT-2003 (TrEMBLrel. 25, PRELIMINARY; NCBI_TaxID=10116 MAFA protein. 064335 RESULT 1 264335 ACCOCCOS DITAL SERVICE

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--LVLCQSEWLKYQGKCYWFSNEMKSWSDSYVYCLERKSHLL 100
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                                                                                                                                                                                                                                                                       121 LFQEYVGEDFYWIGLRDIDGWRWEDGPALSISILSNSVVQKCGTIHRCGLHASSCEVALQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TFPDNQGVNLFQEYVGE-DFYWIGLRDID---GWRWEDGPALSLSIL-----SNSVVQ 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---GLLTVILM 51
                                                                                                                                                                                                                                                                                                           1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL
                                                                                                                                                   CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFFDNQGVN
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                                MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Human KIRPL, a novel member of the killer cell lectin-like receptor gene family: molecular characterization, genomic structure, physical mapping to the NK gene complex and expression analysis.";

Bur. J. Immunol. 30:568-576(2000).

EMBL, AF175207, AAF37805.1;

GO; GO:0016020; C:membrane; TAS.

InterPro; IPR001304; Lectin_C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20135860; PubMed=10671213;
Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kucherlapati R.,
Fernandez-Ruiz E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 181;
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
receptor F1, splice variant 1 KLRF1-s1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
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nes 51; Conservative
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01-OCT-2000 (
01-JUN-2003 (
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054708
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MEDLINE=99077194; PubMed=9862378;
Hanke T., Corral L., Vance R.E., Raulet D.H.;
"2F1 antigen, the mouse homolog of the rat '$1', is a lectin-like type II transmembrane receptor expressed by natural killer cells.";
Eur. J. Immunol. 28:4409-4417(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=129/SvevTACfBr; TISSUE=Spleen;
MEDLINE=21115136; PubMed=11220622;
Voehringer D., Kaufmann M., Pircher H.;
"Genomic structure, alternative splicing, and physical mapping of the killer cell lectin-like receptor Gl gene (KLRG1), the mouse homologue
                                                                                                                                                                MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
                                                                                                                                                                                                                                                                                                                                                                                                              LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQ
                                                                                                                   1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
                                                                                                                                                                                                                                                 CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN
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01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mast cell function-associated antigen 2F1 (MAFA) (Killer cell lectin-like receptor G1).
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                                                             Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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   11; Length 188;
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                                                             Indels
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EMBL; AR097357; AAD03718.1; -

EMBL; A7010751; CAAD0342.1; -

EMBL, A71727; AAK40082.1; -

MGD; MGI:1355294; KIrgl.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:000529; F:sugar binding; IEA.

GO; GO:007157; P:heterophilic cell adhesion; IEA.

InterPro; IPRO1304; Lectin.C;

Ffam; PRO0559; lectin.C;

Ffam; R000059; lectin.C;

Ffam; R000059; lectin.C;

Ffam; CACOCOSS (LECTI).
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100.0%; Score 1036; DB 1:
100.0%; Pred. No. 1e-102;
ive 0; Mismatches 0
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SEQUENCE OF 2-188 FROM N.A.
Blaser C.;
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Matches 151; Conservative
                                                             188; Conservative
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                                Similarity
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Query Match
Best Local S
Matches 188
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EMBL; AF139769; AAF02492.1; -.
EMBL; AK036697; BAC29537.1; -.
MGD; MGI.145151; Clecsf5.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005529; F:sugar binding; IEA.
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   STRAIN=C57BL/6J; TISSUE=Mammary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50041; C_TYPE_LECTIN_2; 1. PROSITE; PS00022; EGF_1; 1.
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STRAIN-ECSTBL/60, TISSUE-Bone,
MEDIINE=22354683; PubMed=12466851;
The FANTOM CONSORTIUM,
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Best Local Similarity
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98124458; PubMed=9464811;
Vance R.B., Tanamachi D.M., Hanke T., Raulet D.H.;
"Cloning of a mouse homelog of CD94 extends the family of C-type
lectins on murine natural killer cells.";
Eur. J. Immunol. 27:3236-3241(1997).
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Heusel J.W., Ho E.L., Brown M.G., Matsumoto K., Yokoyama W.M.;
"Murine CD94.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Killer cell lectin-like receptor, subfamily D, member 1 (CD94).
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                                                                                         Last sequence update)
Last annotation update)
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Vance R.E., Tanamachi D.M., Hanke T., Raulet D.H.;
Bur. J. Immunol. 27:0-0(1997).
   179 AA
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GO; GO:005529; F:sugar binding; IEA.
InterPro; IPR006209; EGF like.
InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
PROSITE; PS50041; CIYPE LECTIN_Z; 1.
PROSITE; PS00022; EGF_1; 1.
                                                            Created)
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PRELIMINARY;
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                                                                                                                                                                               KLRD1 OR CD94.
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79 WMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGL--- 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 SRWKVKAVLHR-PCVSYLVMVALGLLTVILMSLLLYQRTLC-CGSKGFM-CSQCSRCPNL 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 RDIDGWRWEDGPALSLSILSN-SVVQKCGTIHRC-----GLHASSCEVALQWICEKV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 EKRNAWLWEDGITVPSKDLFPEFSVIRP----EHCIVYSPSKSVSAESCENKORYICKKL, 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=BALB/C; TISSUE=Myeloid; MEDLINE=99380598; PubMed=10449773; Bakker A.B., Baker E., Sutherland G.R., Phillips J.H., Lanier L.L.; "Myeloid DAP12-associating lectin (MDL)-1 is a cell surface receptor linvolved in the activation of myeloid cells."; Proc. Natl. Acad. Sci. U.S.A. 96:9792-9796(1999).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Butcher S., Cottage A., Cook G.D., "Mouse natural killer cell receptors homologous to human CD94 and NKG2-D.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
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                                                                                   (DEC-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 AA; 20808 MW; DD343419E93B3465 CRC64;
                                                                                                       Last annotation update)
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Receptor.
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                                                                                                                                                             92 EKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGLRDIDG---WRWEDGPA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 SENSWANSWAPCKQKGSTLAIVNTPEKLKFLQNISGAEKYFIGLLYQPAEKOMRWINNSV 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
                                                                                                                  86 CYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGLRDIDG---WR
                                                                                                      ----- ORTLCCGSKGFMCSQCSRCPNLWMRNGSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 MIISGLIVVVLKIVGMTFFLLYFPQIFGSSNVSFTPTESFGTVCPTGWDFHQGRCFFLST
                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21308528; PubMed=11414735;
Yim D., Jie H.B., Sotiriadis J., Kim Y.S., Kim Y.B.;
"Molecular cloning and expression pattern of porcine myeloid DAP12-associating lectin-1.";
                                                                                                                                                                                                                                                                                                                               Sūs scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                  30;
                                                            ; Score 173; DB 11; Length 165; ; Pred. No. 1.9e-10; 28; Mismatches 61; Indels 3
                                                                                                                                                                                         143 WEDGPALSLSILSNSVVQKCGTIHRCGL----HASSCEVALQWICE 184
                                                                                                                                                                                                    Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69; Indels
                                        165 AA; 19055 MW; 626D64392A513282 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIGSVISHSHNFNCVTI---GLTKTFDAASCDVNYRSICEK 162
                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
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EMBL; AF288449; AAG29427.1; -

GO; GO:0005529; F:sugar binding; IEA.

GO; GO:0007157; F:heterophilic cell adhesion; IEA.

InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.5%; Score 171; DB 6;
29.2%; Pred. No. 3.1e-10;
ative 27; Mismatches 69;
                                                                                                                                                                                                                                                                                                                     Myeloid DAP12-associating lectin short form.
                                                                                                                                                                                                                                                                  165 AA.
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     SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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                                                                                                      40 MVALGLLTVILMSL----LLY
                                                            16.7%;
28.3%;
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                                                                                 47; Conservative
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                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9823;
                              Transmembrane
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01-MAR-2001 (
01-OCT-2003 (
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Q8BL24;
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86 CYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGLRDIDG---WR 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 MVALGLLTVILMSL----LLY-----QRTLCCGSKGFMCSQCSRCPNLWMRNGSH 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=273EL/61; TISSUE=Adipose tissue;
MEDLINE=2354683; PubMed=12466851;
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 7.70 full-length CDNAs.";
Mature 420:563-573 (2002).
BMBL; AKO46600; BAC32802.1;
GO; GO:0005529; F:sugar binding; IEA.
InterPro; IPR001304; Lectin_C.
SMART; SM00034; CLECT; 1.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinee; Bos.
                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Goverts M.M., Goddeeris B.M.;
"Homologues of natural killer cell receptors NKG2-D and NKR-P1
expressed in cattle.";
Vet. Immunol. Immunopathol. 80:339-344 (2001).
EMBL; AF322886; AAK73811.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Natural killer cell receptor protein 1 variant 1 (Fragment)
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SEQUENCE 164 AA; 18927 MW; DF0AE012C049CIC0 CRC64;
Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.0%; Score 165.5; DB 1.
28.9%; Pred. No. 1.2e-09;
ive 28; Mismatches 59
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GO; GO:0005529; F:sugar binding; IEA.
InterPro; IPR001104; Lectin_C.
Ffam; PF00059; lectin_G; 1.
SMART; SM00034; CLECT; 1.
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01-DEC-2001 (TrEMBLrel. 19, Last seq
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MEDLINE=21351526; PubMed=11457486;
(TrEMBLrel. 23, TrEMBLrel. 23, TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                               C-type.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                        NCBI_TaxID=10090;
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                         01-MAR-2003
01-OCT-2003
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PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=Testis;
                                                                                                              POPY-CD94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8WUP7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
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                                                                                                                                                  75 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLITFPDNQGVNLFQEYVGED--FYW 132
                                                                                                                                                                                  IGLR-DIDG--WRWEDGPALS---LSILSNSVVQKCGTIHRCGLHASSCEVALQWICEKV 186
                                                                                                                                                                                                                                                                               101 IGLNFTLSGKSWKWINGSFLNSNILPIFGDAKEDCCVYISKTQCISDYCAAKNRWICQKE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFY 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 WIGLRDIDG---WRWEDGPALSLSILSNSVVQKCGTIHRCGL----HASSCEVALQWICE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 MIISGLIVVVLKIVGMTFFLLYFPQIFGEHNVSFSPTERPGTVPQIFGSSNVSFTPTESF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21308528; PubMed=11414735;
Yim D., Jie H.B., Sotiriadis J., Kim Y.S., Kim Y.B.;
"Molecular cloning and expression pattern of porcine myeloid DAP12-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sús scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38;
                                                                 Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6; Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 15.8%; Score 164; DB 6; Length 18
1 Similarity 27.1%; Pred. No. 2e-09;
49; Conservative 22; Mismatches 72; Indels
  161
18648 MW; 24F9AA44A19EAFB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20835 MW; DA6ECOAF58BC95CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell. Immunol. 209:42-48 (2001).

EMBL; AF2845450, AAG29428.1, -.

GO; GO:0005529; F:sugar binding; IEA.

GO; GO:0007157; P:heterophilic cell adhesion; IEA.

InterPro; IPRO01304; Lectin_C.

FRam; PF00059; lectin_C; 1.

FRAMR; SM00034; CLECT; 1.

PROSITE; PS50041; C_TYPE_LECTIN_Z; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 MVALGLITVIL----MSLLLYQRTLCCGSKGFMCSQCSR-
                                                             15.9%; Score 165; DB 6;
ilarity 31.4%; Pred. No. 1.3e-09;
Conservative 19; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence u
01-OCT-2003 (TrEMBLrel. 25, Last annotation
Myeloid DAF12-associating lectin long form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              associating lectin-1
  161
161 AA;
                                                                                   Local Similarity
ses 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                          187 L 187
                                                                                                                                                                                                                                                                                                                                                                       161 L 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 K 185
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NON TER
SEQUENCE
                                                                                                                                                                                                                                        133
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                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9GLF3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
Q8MHY8
ID Q8MHY
                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FT
                                                                                                                                                                                       Db
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79 WMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGL--- 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-22072192; PubMed=12077248; Guethlein L.A., Flodin L.R., Adams E.J., Parham P.; Apivotal Wink Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 WKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTLCCG----SKGFMCSQCSRCPNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 WLISGTLGIICLS--LMATLGILLKNSFTKLSIEPAFTPGPDIELOKD---SDCCSCOEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 RDIDGWRWEDGPALS---LSILSNSVVQKCGTIHRCG-LHASSCEVALQWICEKVL 187
                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
NCBI TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R., Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 AA; 20550 MW; 6752CB8F182CFD73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Natural killer cell receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
15.6%; Score 161.5; DB 6
Best Local Similarity 27.3%; Pred. No. 3.6e-09;
Matches 48; Conservative 25; Mismatches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-007-2003 (TrEMBLrel. 25, Last anotationallar to lectin-like NK cell receptor. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Immunol. 169:220-229(2002).

BMBL; AP470381; AAM78481.1;

EMBL; AP470382; AAM78482.1;

GO; GO:0004872; F:receptor activity; IEX

GO; GO:0005529; F:receptor activity; IEX

INTERPRO; IPR006209; EGF like.

INTERPRO; IPR001304; Lectin...

PFAM; PR00134; CLECT...

PROSITE; PS50041; C.TYPE LECTIN.2; 1.

PROSITE; PS50041; C.TYPE LECTIN.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                             Pongo pygmaeus (Orangutan)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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Pfam; PF00059; lectin c; 1. SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                SEQUENCE FROM N.A.
Mueller A., Merz H.,
"Expression of MDL-1
Submitted (JAN-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ICEK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ICEK 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8MJI3
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Q8MJI3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
qq
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                                                                                                                                                                                                                                         CSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGE 128
                                                                                                                                                                                                                                                                     SRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCA-DKGSHLLTFPDNQGVNLFQEYVGEDFY 131
                                                                                                                                                      68
                                                                                                                                                                                                69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Yim D., Sotiriadis J., Kim K.-S., Shin S.-C., Jie H.-B.,
Rothschild M.F., Kim Y.B.;
"Molecular cloning, expression pattern, and chromosomal mapping of pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 WIGLRDIDG--WRWEDGPALSISI-LSNSVVQKCGTIHRCGLHASSCEVALQWICEK 185
                                                                                                                                                                                  42 SSCPDDWIGYQTKCYFISKKTKNWTLAQSFCSKHHGATLALLESKEDMVFLKQHVGRAEH
                                                                                                                                                    11 ELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLL--LYQRTLCCGSKGFM
                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
Sus.
                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 15.4%; Score 160; DB 6; Length 159; Best Local Similarity 28.2%; Pred. No. 4.5e-09; Matches 33; Conservative 27; Mismatches 51; Indels
                                                                Length 154;
                                                                                                        67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF484234; AAL91547.1; -... AP484234; AAL91547.1; -... AC, 600.005529; F: sugar binding; IEA.
InterPro; IPR001304; Lectin_C;
Pfam; PF00059; lectin_c; 1... SMART; SM00034; CLECT; 1... TYPE LECTIN 2; 1... PROSITE; PS6014; C TYPE LECTIN 2; 1... SEQUENCE 159 AA; -18056 MW; Ā19C3EEBAE92AA69 CRC64;
                    154 AA; 17728 MW; 7771926F318C038D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-UTN-2002 (TrEMBLrel. 21, Created)
01-UTN-2002 (TrEMBLrel. 21, Last sequence update)
01-UTN-2003 (TrEMBLrel. 25, Last annotation update)
Type II membrane protein CD69 splice variant.
Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                            15.4%; Score 160; DB 4; 28.6%; Pred. No. 4.3e-09; iive 23; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 AA
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                                                                                                          40; Conservative
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                                                                                   Similarity
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                                                            Query Match
                    SEQUENCE
                                                                                     Local
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MEDLINE=22072192; PubMed=12077248;

Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;

Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;

Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors with MHC-C.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----KGEMCS
                                                                                                                                                                                                                                                                                Bakker A.B., Baker E., Sutherland G.R., Phillips J.H., Lanier L.L.;
Bakker A.B., Baker E., Sutherland G.R., Phillips J.H., Lanier L.L.;
"Myeloid DAP12-associating lectin (MDL)-1 is a cell surface receptor involved in the activation of myeloid cells.";
Proc. Natl. Acad. Sci. US.A. 96:9792-9796(1999).
BMEL; AJ271684; CAB71334.1; -.
BMEL; AJ271684; CAB71334.1; -.
GO; GO:0007157; P:sugar binding; IEA.
GO; GO:0007157; P:heterophilic cell adhesion; IEA.
InterPro; IPR001594; Lectin. C.
Pfam; PR00059; lectin. C.
SMART; SM00034; CLECT; 1.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 188;
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Feller A.C.; in human blood and cell lines."; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 AA; 21521 MW; 94A2DBD520DC1985 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.4%; Score 159.5; DB 4
25.5%; Pred. No. 6.2e-09;
ive 31; Mismatches 65
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POPY-CD94.
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79 WMRNGSHCYYFSMEXRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGL--- 135
                                                                                                                                                                                                                        24 WKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTLCCG-----SKGFMCSQCSRCPNL 78
                                                                                                                                                             10 WLISGTLGIICLS--LMATLGILLKNSFTKLSIEPAFTPGPDIELQKD---SDCCSCQEK 64
                                                                                                                                                                                                                                                               Query Match 15.3%; Score 158.5; DB 6; Length 179; Best Local Similarity 26.7%; Pred. No. 7.5e-09; Matches 47; Conservative 26; Mismatches 84; Indels 19; Gaps
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PROSITE; PS00022; EGF_1; 1.
Receptor.
SEQUENCE 179 AA; 20566 MW; 6752CB9F0F9A2609 CRC64;
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Search completed: August 10, 2004, 16:44:03 Job time : 32 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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sw model using - protein search, OM protein

August 10, 2004, 16:35:35; Search time 47.5 Seconds (without alignments) 1118.293 Million cell updates/sec Run on:

US-09-811-367B-5 1036 1 MADNSIYSTLELPAAPRVQD......GLHASSCEVALQWICEKVLP 188 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1082526 Total number of hits satisfying chosen parameters:

282547505 residues

1586107 seqs,

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 188

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A Geneseq 29Jan04:* geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:* 6: 7: 8: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	ion	Aar77033 Mammalian	Aaw88277 Rat mast	Aael1761 Rat mast	0 Mous		Aaw88267 Human MAF	Aau00673 Human INT	Abo32541 Secreted	Aau19660 Human nov	Abp47880 Human pol	Human	Aam80296 Human pro	Abg72616 Human cyt	Human	Aau00675 Human INT	7	Aaw27288 Human G52	Adc38664 Human sec	Aay27446 Human SDC	Aam78675 Human pro		Abo32533 Secreted	N	Aaw36957 Protein e	Aaw64791 Human Kp4
SUMMAKIES	Ωï	AAR77033	AAW88277	AAE11761	AAE11760	AAR77472	AAW88267	AAU00673	AB032541	AAU19660	ABP47880	ADC10842	AAM80296	ABG72616	AAM80302	AAU00675	AB032547	AAW27288	ADC38664	AAY27446	AAM78675	AAU00671	AB032533	AAW63022	AAW36957	AAW64791
	DB	7	7	4	4	7	7	4	9	4	Ŋ	7	4	9	4	4	9	C)	7	N	4	4	9	~	ď	7
	Query Match Length	188	188	188	188	114	66	165	165	182	182	182	142	142	160	145	145	181	181	162	188	188	188	167	149	179
*	Query Match	100.0	100.0	100.0	80.9	62.8	20.0	16.4	16.4	15.9	15.9	'n		15.8	15.8	15.7	15.7	15.5	15.5	15.4	15.4	15.4	15.4	15.3	15.1	15.0
	Score	1036	1036	1036	838	651	207.5	170	170	164.5	164.5	164.5	163.5	163.5	163.5	163	163	191	161	160	159.5	159.5	159.5	58.	156.5	155
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Gaps

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Length 188; Indels

Query Match 100.0%; Score 1036; DB 2; Best Local Similarity 100.0%; Pred. No. 1.8e-96; Matches 188; Conservative 0; Mismatches 0;

Sequence 188 AA;

	Abo32535 Secreted Aau19836 Human nov Aau19690 Human nov	Abb15422 Human ner Abb17909 Human ner Abp48056 Human pol	Human	Human Type I	Adwassyz Human C-c Abb09713 Amino aci Adc38674 Human sec	Aaw63013 Mouse dec Aau72822 Human NKG Aau72821 Human NKG
AAW40222 ADE76965 ABO32543	ABO32535 AAU19836 AAU19690	ABB15422 ABB17909 ABP48056	ABP47910 ADC10872 ADC11018	ADCII 010 AAW64544 AAW75877	AAM85592 ABB09713 ADC38674	AAW63013 AAU72822 AAU72821
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155 155 154	154 153.5 153.5	153.5 153.5 153.5	153.5 153.5	153.5	153.5 153.5	153 153 153
26 27 28	30 31	332 432	36	. B B C	4 4 4 2 1 2	4 4 4 4 4 5

ALIGNMENTS

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Mast cell function-associated antigen, MAFA, soluble, ligand, identification; screening; inflammation; inflammatory; allergy; allergic; prevention.
                                                                                                                                                                                                                                                                                                                                                                                                             Novel DNA encoding a mast cell function-associated antigen (MAFA) - useful for screening for ligands of MAFA which are useful for prevention of inflammatory and allergic reactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A soluble form of mast cell function-associated antigen (MAFA) can be produced by recombinant techniques for use in the ligand- screening assay. The ligands that are identified may be used alone or in combination with the MAFA to prevent inflammatory and allergic reactions
                                                                                          Mammalian mast cell function-associated antigen (MAFA).
             AAR77033 standard; protein; 188 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; Page 37; 54pp; English.
                                                                                                                                                                                                                                                                                                                                               Tal M;
                                                                                                                                                                                                                                                                                                      (YEDA ) YEDA RES & DEV CO LTD (RYCU/) RYCUS A.
                                                                                                                                                                                                                                                                                94IL-00109257.
                                                                                                                                                                                                                                                      95WO-US004258.
                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-366356/47.
                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAT01471
                                                                                                                                                                         Rattus rattus.
                                                                                                                                                                                                 W09527734-A1.
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                                                                                                                                                                                                                                                                              08-APR-1994;
                                                                                                                                                                                                                            19-0CT-1995.
                                                                  01-FEB-1996
                                         AAR77033;
AAR77033
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New polypeptide having a sequence corresponding to human mast cell function-associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic
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                                                                                                                                9
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9
                1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLIVILMSLLLYQRTL
                                                                       CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN
                                                       CCGSKGFMCSOCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNOGVN
                                                                                                              LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQ
MADNSIYSTLELPAAPRVODDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYORTL
                                                                                                                                                                                                                                                                                                                                                                                    Mast cell function-associated antigen; MAFA; splice variant; rat; inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.
                                                                                                                                                                                                                                                                                                                                                         cell function-associated antigen (MAFA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82. .84
/note= "Asn is N-glycosylated"
97. .99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                    AAW88277 standard; protein; 188 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PEPT-) PEPTIDE THERAPEUTICS LTD.
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                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                        WICEKULP 188
                                                                                                                                                                     WICEKVLP 188
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Sequence 188 AA;

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The present invention relates to a pharmaceutical composition comprising an agent which specifically binds to a mast cell function associated antigen (MARA) ligand on a target cell, and prevents or inhibits natural killer (NK) - or T-cell-expressed cell surface MARA from binding to MARA tigand and a pharmaceutically acceptable excipient. The invention is cueful for inhibiting an NK- or T-cell-expressed cell surface MARA binding to a ligand on a target cell. by contacting the pharmaceutical composition in vitro, ex vivo or in vivo by administering the composition and amount sufficient to inhibit cell surface MARA binding to the ligand on the target cell. The agent or the composition is useful for treating a newour by stimulating the cyctoxic activity of an NK cell- or a cytotoxic T-cell (CTL), where the tumour comprises an NK cell- or TL-susceptible tumour cell. The invention is also useful for inhibiting an activity of NK cell or a T-cell. The present sequence is rat MARA protein
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                                                                                                                                          120
                                                                                                                                                                                                               180
                                                                                                                                                                  61 CCGSKGFMCSQCSRCPNLWMRNGSHCXYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pharmaceutical composition for treating tumor by stimulating cytotoxic activity of natural killer cell or T-cell, comprises an agent that binds to mast cell function-associated antigen ligand on target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat; pharmaceutical composition; mast cell function associated antigen; MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL; immunosuppressive; cytostatic.
                                                                                                                                            CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN
                                                                                                                                                                                                                 121 LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQ
                                                                    1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
                                                                                                       1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
                                     Gaps
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0
Length 188;
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat mast cell function associated antigen (MAFA) protein.
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Score 1036; DB 2;
Pred. No. 1.8e-96;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                               AAE11761 standard; protein; 188 AA.
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                                     0;
 100.0%;
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                                     188; Conservative
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                  Similarity
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Best Local
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to the subject, to NK or T-cell or the target cell e.g. tumour cell, in an amount sufficient to inhibit cell surface MAFA binding to the ligand on the target cell. The agent or the composition is useful for treating a tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic T-cell (CTL), where the tumour comprises an NK cell or CTL-susceptible tumour cell. The invention is also useful for inhibiting an activity of NK cell or a T-cell. The present sequence is mouse MAFA protein
                                                                                                                                                                                                                                                                                                                                                                                                                          CGGSKDSTCSHCPSCPIIMTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120
                                                                                                                                                                                                                                                                                                                                                                                                 61 CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALO 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mast cell function-associated antigen, MAFA, soluble, ligand, identification, screening, inflammation, inflammatory, allergy, allergic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel DNA encoding a mast cell function-associated antigen (WAFA) - useful for screening for ligands of MAFA which are useful for prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A soluble form of mast cell function-associated antigen (MAFA) can be produced by recombinant techniques for use in the ligand- screening assay. The ligands that are identified may be used alone or in combination with the MAFA to prevent inflammatory and allergic reactions
                                                                                                                                                                                                                                                                                                                                                    1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL
                                                                                                                                                                                                                                                                                                              1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYORTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Partial sequence of mast cell function-associated antigen (MAFA)
                                                                                                                                                                                                                        Length 188
                                                                                                                                                                                                                                                                 21; Indels
                                                                                                                                                                                                                        80.9%; Score 838; DB 4;
80.7%; Pred. No. 1.9e-76;
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                                                                                                                                                                                                                                            Best_Local Similarity 80.7
Matches 151; Conservative
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                                                                                                                                                                             Sequence 188 AA;
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                                                                                                                                                                                                                                        CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120
                                                                                                                                                                                                                                                                                                                           LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQ 180
                                                                                                                                                                                                                                                                                                                                                    Mouse; pharmaceutical composition, mast cell function associated antigen, MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
                                                                                                                                                                                                                                                                              CCGSKGFMCSQCSRCPNLMMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120
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                                                                                                                                                                                      1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
                                                                                                                                                    1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
                                                                                                              0;
                                                                 Length 188;
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                                                                                                            Indels
                                                                 5; DB 4;
1.8e-96;
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                                                            100.0%; Score 1036;
100.0%; Pred. No. 1.8
:ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunosuppressive; cytostatic.
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                                                                                                            Conservative
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                                                                              Local Similarity
nes 188; Conserv
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                      Sequence 188
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18-DEC-2001 Mouse mast

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide having a sequence corresponding to human mast cell function-associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic
                                                                                              CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is the amino acid sequence of human mast cell function- associated antigen (MAPA) splice variant huMAFA(B3/4-), which lacks the C-lectin-like domain of human MAPA (see AAM88265) but retains the intracellular and transmembrane domains as well as the extracellular C-terminal tail. Truncated MAPA polypeptides including huMAFA(B3/4-), and polynucleotides encoding them, as well as synthetic peptides (see AAW88258-64, AAW88268-72), can be used be used in compositions for the treatment of inflammatory and allergic diseases (e.g. rheumatoid arthritis and asthma), or tumour growth
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                                                                                                                          CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIG
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                                                                                                                                                                        LRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQWICEKVLP 114
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                                                                                                                                                                                                                                                                                                                                                                 Mast cell function-associated antigen; MAFA; huMAFA(E3/4-); splice variant; human; inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.
                                      Length 114;
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                                                                  Indels
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                                                     8.1e-58;
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29.6%; Pred. No. 4.7e-13;
tive 12; Mismatches 30
                              62.8%; >cc...
100.0%; Pred. No. c...
0; Mismatches
                                       DB
                                                                                                                                                                                                                                                                                                                                     Human MAFA splice variant huMAFA(E3/4-).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PEPT-) PEPTIDE THERAPEUTICS LTD.
                                                                                                                                                                                                                                                      AAW88267 standard; protein; 99
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                                                                  Natches 114; Conservative
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N-PSDB; AAV84200.
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                                                     Similarity
             Sequence 114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 99 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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The sequence represents human INTERCEPT 289 form 2a polypeptide. This protein and similar others exhibit the ability to affect growth, proliferation, survival, differentiation, activity, morphology, or movement/migration of, e.g. T cells and cells of the heart, liver, pancreas, placenta, brain, lung, skeletal muscle, kidney, spleen, lymph node, peripheral blood leukocyte, bone marrow or thymus tissue. They can be used as modulating agents for regulating cellular processes, thus, the proteins and their associated nucleic acids can be used to prognosticate, prevent, diagnose, or treat disorders associated with physiological processes. These disorders include abnormal blood coagulation, asthma, anaphylaxis, hepatitis, multiple sclerosis, cancer, coronary artery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid molecule for diagnosis, prevention, and therapy of human and other animal disorder, or as modulating agent for regulating
CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120
                                                                           121 LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQ 180
                                                                                                                   --ISSNSFVQTCGAITKNGLQASSCEVPLH 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    skeletal muscle, kidney; spleen; lymph node; peripheral blood leukocyte; bone marrow; thymus tissue; abnormal blood coagulation; asthma; cancer; anaphylaxis; hepatitis; multiple sclerosis; coronary artery disease; malaria; atopic dermatitis; amyotrophic lateral sclerosis; meningitis; attention deficit disorder; Crohn's disease; gastroenteritis; goltre; hypoglycaemia; diabetes mellitus; endometriosis; pulmonary embolism; muscular dystrophy; immuno-competence; vertebrate; blood; serum; lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERCEPT 289; T cell; heart; liver; pancreas; placenta; brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leiby KR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser CC,
                                                                                                                                                                                                                                                                                                                                                                                                                             Human INTERCEPT 289 form 2a polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Fig 2H-2I; 263pp; English.
                                                                                                                                                                                                                                                                                                       AAU00673 standard; protein; 165 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kirst SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-00420707.
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                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-308477/32.
                                                                                                                                                              181 WICEKV 186
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hormonal disorder; proliferative disorder; cancer; thyroid disorder;
diabetes; multiple sclerosis; lupus; neurological disorder; anaemia;
Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
myocardial infarction; congestive heart disease; blood platelet disorder;
thrombocytopenia; blood vessel; atherosclerosis; vasculitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 EKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGL---RDIDGWRWEDGPA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SESSWINESRDFCKGKGSTLAIVNTPEKLKFLQDITDAEKYFIGLIYHREEKRWRWINNSV 124
disease, malaria, atopic dermatitis, amyotrophic lateral sclerosis, meningitis, attention deficit disorder, Crohn's disease, gastroenteritis, goitre, hypoglycaemia, diabetes mellitus, endometriosis, pulmonary embolism and muscular dystrophy. Antibodies to disorders such as these can be made by providing a polypeptide of the invention to an immunocompetent vertebrate and harvesting blood or serum from the vertebrate
                                                                                                                                                                                                                                                                                                                                                                             40 MVALGLLTVIL-----MSLLLYQRTLCCGSKGFMCSQC--SRCPNLWMRNGSHCYYFSM 91
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                            16.4%; Score 170; DB 4; Length 165; 27.3%; Pred. No. 5.5e-09;
                                                                                                                                                                                                                                                                                                                     68; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 FNGNVTNQNQNFNCATI---GLTKTFDAASCDISYRRICEK 162
                                                                                                                                                                                                                                                                                                                     31; Mismatches
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10-SEP-1999; 99US-0033996.

19-OCT-1999; 99US-00420707.

07-JAN-2000; 2000US-00479249.

27-APR-2000; 2000US-00559497.
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                                                                                                                                                                                                                                                                                                                        Conservative
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GOODEARL A D
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BARNES T M.
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KIRST S J.
MYERS P S.
LEIBY K R.
                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                       Sequence 165 AA;
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(BARN/)
(SHAR/)
(KIRS/)
(MYER/)
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(HOLT/)
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(MACK/)
(GOOD/)
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                                                                                                                                                                                                                                                                                                                  Matches
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The invention relates to secreted polypeptide-related proteins and nucleic acids (TANGO and INTERCEPT proteins and nucleic acids). The nucleic acids, proteins and antibodies specific to the proteins are nucleic acids, proteins and antibodies specific to the proteins are useful in screening assays, predictive medicine (e.g. diagnostic assays, proprostic assays, proprostic assays, monitoring clinical trials and pharmacogenetics) and propristic assays, monitoring clinical trials and pharmacogenetics) and diagnosing, preventing or treating proliferative disorders (e.g. anultiple sclerosis or lugus), neurological disorders (e.g. multiple sclerosis or lugus), neurological disorders (e.g. Alzheimer's disease or Parkinson's disease), cardiovascular clisorders (e.g. promocardial infarction or congestive heart disease), blood platelet disorders (e.g. thrombocytopenia or anaemia) and disorders involving blood vessels (e.g. thrombocytopenia or anaemia) and disorders acids may also be used in chromosome mapping, tissue typing and forensic bology, and as surrogate markers. This sequence represents a secreted polypeptide-related protein of the invention. Note: The sequence data for this patent was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 EKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGL---RDIDGWRWEDGPA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 SESSWNESRDFCKGKGSTLAIVNTPEKLKFLQDITDAEKYFIGLIYHREEKRWRWINNSV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted extracellular matrix protein; immunomodulatory; Anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 MVALGLLTVIL-----MSLLLYQRTLCCGSKGFMCSQC--SRCPNLWMRNGSHCYYFSM 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antianemic; antirheumatic; antisclerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytostatic; antialzheimers; immune/autoimmune disease; HIV infection; anaemia; human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis; cancers; hyperproliferative disorder; breast neoplasm; melanoma;
                                                                                                                                                     TANGO 210 or INTERCEPT 217), useful for diagnosing, preventing or treating disorders such as cancer, diabetes or atherosclerosis, and in forensic biology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid molecule encoding a secreted protein (e.g. TANGO 202,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sezary syndrome, Gaucher's disease; neurological diseases; Alzheimer's disease; Parkinson's disease; cardiovascular disorder; cardiac arrest; tachycardia; angina; infection; corneal infections; wound healing; immunogen; gene therapy; antisense; food additive.
                  Sharp JD, Kirst SJ, Myers PS, Leiby KR;
SA, Wrighton N, Mackay CR, Goodearl ADJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 165;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human novel extracellular matrix protein, Seg ID No 310.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.4%; Score 170; DB 6; 27.3%; Pred. No. 5.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31; Mismatches
                                                                                                                                                                                                                                                                 Claim 9; Fig 11H-11K; 482pp; English.
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                                                                                    WPI; 2003-456290/43.
N-PSDB; ACD66723, ACD66724
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nes 44; Conservative
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                                          Mccarthy
                  Barnes
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DA,
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                                          Holtzman
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                            produce antibodies and to identify modulators (agonists and antegonists) of the SPs. The anti-(SP) antibodies and antagonists may also be used to down regulate expression and activity of SP and as diagnostic agents for detecting the presence of SPs in samples. The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease), neurological diseases (e.g. Alzheimer's disease, Parkinson's disease) cardio-forebrowscular disorders (e.g. cardiac arrest, tachycardia and angina), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). Other uses include wound healing, maintenance of organs before transplantation, support of cell culture of primary
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                                                                                   Nucleic acid molecules encoding human secreted extracellular matrix proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers.
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                                                                                                                                               Claim 11; SEQ ID NO 310; 577pp; English.
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            Ruben SM;
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nucleic acid encoding human proteins, useful for diagnosis, treatment prevention of e.g. osteoporosis, also related polypeptides and
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medical conditions e.g. by protein or gene therapy. The genes are solated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and over cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or unogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune heamolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as mycocardial isohaemias; (d) wound healing (c) cardiovascular diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 15.9%; Score 164.5; DB 5; Length 182; Best Local Similarity 26.9%; Pred. No. 2.2e-08; Matches 36; Conservative 22; Mismatches 59; Indels 17; Gaps
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                                                                                                                                                                                                                                                                                                                                       from USPTO at seqdata.uspto.gov/sequence.html?DocID=999909764870
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04-FEB-2000; 2000US-0184664P.
02-MAR-2000; 2000US-0184664P.
16-MAR-2000; 2000US-0189350P.
17-MAR-2000; 2000US-0189374P.
18-APR-2000; 2000US-019131P.
19-MAY-2000; 2000US-019123P.
19-MAY-2000; 2000US-0205515P.
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2000US-0241785P

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The invention relates to an isolated nucleic acid molecule (CDNA) encoding a human extracellular matrix protein, representing one of 161 novel genes. Also include are recombinant vectors, host cells (expressing the protein), the extracellular matrix proteins (including
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2000US-0249210P.
2000US-0249211P.
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2000US-0249217P.
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                                     2000US-0241809P.
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2000US-0246474P.
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their fragments, epitopes and homologues), an isolated antibody that binds specifically to the protein, diagnosing a pathological condition or susceptibility to a pathological condition (comprising determining the presence or absence of a mutation in the mucleic acid and diagnosing a condition based on the presence or absence of the mutation), diagnosing a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or protein in a biological sample and diagnosing a condition based on the presence or amount of expression of the protein), preventing, treating presence or amount of expression of the protein), preventing, treating or memiliar and mammalian subject, identifying a binding partner to the protein to a mammalian subject, identifying a binding partner to the protein, the gene corresponding to the cDNA sequence, and identifying an ectivity in a biological sasy (comprising expressing the mucleic acid in a cill, isolating the supernatant, detecting an activity in a biological casay and identifying the protein in the supernatant having the activity). The nucleic acids and proteins display the following activity of astrointestinal-den, Cardiant, Cardiovascular-Gen, Gynaecological, Gastcointestinal-Gen, Respiratory-Gen, Nephrotropic, Antiinflammatory, Muscular-Gen, Respiratory-Gen,
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Pang D, Wang J, Zhang J, Ren F,
                                                                                                                                                                                                                                                                                                                                                               15.9%; Score 164.5; DB 7; 26.9%; Pred. No. 2.2e-08;
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2000US-00654936.
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2000US-00728422.
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2000US-00598075.
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Ma Y, Zhao QA, Wang D,
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production of other cytokines in other cell populations. The populations of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, nematopoiesis regulating activity, issue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leudaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                   The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   wound; ulcer; thrombocytopaenia; osteoporosis; osteoarthritis; inflammation, Alzbeimer's disease; Parkinson's disease; stroke; Huntington's disease; amyotrophic lateral sclerosis; HIV; immune deficiency; human immunodeficiency virus infection; severe combined immunodeficiency; infection; autorimmune disorder; rheumatoid arthritis; Guillain-Barre syndrome; graff-versus-host disease; cancer; thyroid cancer; lung cancer; small cell carcinoma; Asposi's sarcoma; brain tumour; prostate cancer; ovarian cancer; leukaemia; inflammatory disorder; criflammatory disorder; crohn's disease; food supplement.
                                                                                                            Nucleic acids encoding polypeptides with cytokine-like activities, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 SSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGL-RDIDGWRWEDGPALSLSIL-- 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cytokine or cell proliferation/differentiation protein #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.8%; Score 163.5; DB 4; Length 142; 26.1%; Pred. No. 2.1e-08; ive 25; Mismatches 67; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --SNSVVQKCGTIHRCGLHASSCEVALQWICEK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGEDNLDINCGALEEGTLVAANCSTPRPWVCAK 139
Goodrich R;
                                                                                                                                                                          Claim 20; Page 6210-6211; 6221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG72616 standard; protein; 142 AA.
Yang Y, Wejhrman T,
                                                                                                                                   diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001; 2001US-00774434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-FEB-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 15.8%
Best Local Similarity 26.1%
Matches 40; Conservative
                                       2001-476283/51.
                                                                N-PSDB; AAK53429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2002137044-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG72616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107
Xue AJ,
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
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The invention relates to an isolated polynucleotide encoding a cytokine or cell proliferation/differentiation-related protein (or the mature protein or active domain), sequences greater than 90% identical to it or sequences complementary to it. Also included are the encoded proteins, expression vectors, transformed host cells, antibodies, and identifying compound that binds to the polypeptide. The polymucleotide, polypeptides compound that binds to the polypeptides. They are particularly useful conforded by it, or antibodies to the polypeptides. They are particularly useful conforded by it, or antibodies to the polypeptides. They are particularly useful conforded by it, or antibodies to the polypeptides. Wounds, ulcers, thrombocytopaenia, osteoporosis, osteoarthritis, inflammations, chrombocytopaenia, osteoporosis, stroke, immune deficiency of e.g. human immunedaticiency virus (HIV), severe combined immundeficiency or infections), autoimmune disorders (e.g. rheumacoid arthritis, Guillain-conformed or graft-versus-host disease), cancers, thy conforders (e.g. thyroid cancers, ung cancers, small carcinoma, kaposis, sarcoma, brain cumours, prostate cancer, ovarian cancer or leukaemias), or inflammatory disorders (e.g. inflammatory bowel disease or Crohn's disease). The conformed in hithistory or anyonists that are useful for screening applieds or small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 SSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGL-RDIDGWRWEDGPALSLSIL-- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 ASQAFCSAYHATLPILISHTQ--DFLGRYPVSRHSWVGAWRGPQGWHWIDEAPLPPQLLPE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 LVMVALGLLTVILMSLLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWN 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 VLLAVSGVVIVVLASR----AGAR-----CQQCCPGWVLSEEHCYYFSAEAQAWE 48
                                                                                                                                                                                                                                                                                                                                                               New polynucleotides for diagnosing, treating or preventing e.g. anemia, wounds, ulcers, thrombocytopenia, osteoporosis, inflammations, Alzheimer's disease, stroke, autoimmune disorders or cancers.
                                                                                                                                                                                                                                                 Yang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               molecule inhibitors or agonists that are useful for treating these diseases. The polypeptide is also useful as molecular markers, or a food supplement. The present sequence is a cytokine or cell proliferation/differentiation-related protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                               Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                               Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.8%; Score 163.5; DB 6
26.1%; Pred. No. 2.1e-08;
ive 25; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 --SNSVVQKCGTIHRCGLHASSCEVALQWICEK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 DGEDNLDINCGALEEGTLVAANCSTPRPWVCAK 139
                                                                                                                                                                                                                                               Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM80302 standard; protein; 160 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 19; Page 60; 63pp; English.
                                                                                                                                                                                                                                               Goodrich R,
03-FEB-2000; 2000US-00496914.
27-APR-2000; 2000US-00560875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40; Conservative
                                                                                                                                                                                                                                                                                                        WPI; 2003-110596/10.
                                                                                                                                                                                                       DRMANAC R T.
                                                                              ZHOU P.
GOODRICH R.
                                                                                                                                       ASUNDI V.
WEHRMAN T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                               Zhou P,
                                                           TANG Y T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 142 AA;
                                                                                                                                                                                                                                                                                                                           N-PSDB; ABX13629
                                                                                                                      LIU C.
                                                                                                                                                                                    YANG
                                                                                                                                                                                                                                                                  Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM80302;
                                                                                                                                                                                                                                           rang YT,
                                                                                                                                                                                                     (DRMA/)
                                                                              (ZHOU/)
(GOOD/)
                                                                                                                                                                                  YANG/)
                                                                                                                                                              WEHR/)
                                                           (TANG/)
                                                                                                                                         ASUN/)
                                                                                                                        LIUC/)
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Local Similarity
les 45; Conserve
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                                                                                                                                                                                                                                               Key
             AAU00675
                      The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to oytokine, call proliferation or cell differentiation or which may induce production of other cytokines in other cell appollations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 SSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGL-RDIDGWRWEDGPALSLSIL-- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASOAFCSAYHATLPLLSHTO--DFLGRYPVSRHSWVGAWRGPQGWHWIDEAPLPPQLLPE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 LVMVALGLLTVILMSLLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWN 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----AGAR-----CQQCPPGWVLSEEHCYYFSAEAQAWE 66
                                              Human; cytokine; cell proliferation; cell differentiation; gene therapy;
                                                                                                                                                                                                                                                                                                                             Cao Y;
R, Wang ZW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                  vaccine; peptide therapy; stem cell growth factor; hematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 160;
                                                                                                                                                                                                                                                                                                                               Xu C, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                             RT, Asundi V, Zhou P, Xt
Wang J, Zhang J, Ren F,
n T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.8%; Score 163.5; DB 4 26.1%; Pred. No. 2.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --SNSVVQKCGTIHRCGLHASSCEVALQWICEK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; Page 477; 6221pp; English.
                                                                                                                                                                                                                                                                                                                               Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                      Wejhrman T,
                                                                                                                                                                                                          27-APR-2000; 2000US-00560875.
20-UIN-2000; 2000US-00596075.
19-UUL-2000; 2000US-005235.
01-SIP-2000; 2000US-00654936.
15-SIP-2000; 2000US-00663561.
                                                                                                                                                                                                                                                                     20-OCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00728422.
                      Human protein SEQ ID NO 3960.
                                                                                                                                                                           05-FEB-2001; 2001WO-US004098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 VLLAVSGVVIVVLASR---
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40; Conservative
                                                                                                                                                                                                                                                                                                                                            Wang D,
                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-476283/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                     Yang Y,
                                                                                                                                                                                                                                                                                                                               Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 160 AA;
                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAK53435
                                                                                                                                                                                                                                                                                                                               Tang YT, Liu C
Ma Y, Zhao QA,
                                                                                                                             WO200157190-A2
                                                                                                       Homo sapiens.
                                                                                                                                                                                                  03-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                     Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
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New isolated nucleic acid molecule for diagnosis, prevention, and therapy of human and other animal disorder, or as modulating agent for regulating
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                                                                                                                                                                                                                                                                                                                   Human; INTERCEPT 289; T cell; heart; liver; pancreas; placenta; brain; skeletal muscle; kidney; spleen; lymph node; peripheral blood leukocyte; bone marrow; thymus tissue; abnormal blood coagulation; asthma; cancer; anaphylaxis; hepatitis; multiple sclerosis; coronary artery disease; malaria; atopic dermatitis; multiple sclerosis; coronary artery disease; mattention deficit disorder; Crohn; disease; gastroenteritis; goltre; hypoglycaemia; diabetes mellitus; endometriosis; pulmonary embolism; muscular dystrophy; immuno-competence; vertebrate; blood; serum; lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           can be made by providing a polypeptide of the invention to an immuno-
competent vertebrate and harvesting blood or serum from the vertebrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypoglycaemia, diabetes mellitus, endometriosis, pulmonary and muscular dystrophy. Antibodies to disorders such as these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.7%; Score 163; DB 4;
28.5%; Pred. No. 2.4e-08;
tive 25; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7. .28
/note= "Transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fraser CC,
                                                                                                                                                                                                                                                   Human INTERCEPT 289 form 3a polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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AAU00675 standard; protein; 145 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kirst SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-JUN-2000; 2000WO-US017386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myers PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-308477/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200129088-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-0CT-1999;
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                                                                                                                                                                  07-SEP-2001
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                                                                                 AAU00675;
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9

32;

56; Indels

Conservative

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40 MVALGLITVIL----MSL-LLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKR 94

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1: /cgn2 6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2 6/ptodata/2/pubpaa/PCT NEW PUB.pep:*

3: /cgn2 6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

4: /cgn2 6/ptodata/2/pubpaa/US06 PUBCOMB.pep:*

5: /cgn2 6/ptodata/2/pubpaa/US06 PUBCOMB.pep:*

6: /cgn2 6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

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10: /cgn2 6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

11: /cgn2 6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

13: /cgn2 6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

14: /cgn2 6/ptodata/2/pubpaa/US10A PUBCOMB.pep:*

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16: /cgn2 6/ptodata/2/pubpaa/US10A PUBCOMB.pep:*

17: /cgn2 6/ptodata/2/pubpaa/US10A PUBCOMB.pep:*

16: /cgn2 6/ptodata/2/pubpaa/US10A PUBCOMB.pep:*

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16: /cgn2 6/ptodata/2/pubpaa/US10A PUBCOMB.pep:*

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17: /cgn2 6/ptodata/2/pubpaa/US10A PUBCOMB.pep:*

18: /cgn2 6/ptodata/2/pubpaa/US10A PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                          1036
1 MADNSIYSTLELPAAPRVQD.....GLHASSCEVALQWICEKVLP
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/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                 using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                 - protein search,
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Maximum DB seq length: 188
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                                                                                                                                                     OM protein
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Perfect
                                                                                                                                                                                                                              Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
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Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
-	1036	100.0	188	6	US-09-811-367B-5	Sequence 5, Appli
71	838	80.9		σ	US-09-811-367B-3	Sequence 3, Appli
m	170	16.4		10	US-09-759-130B-98	Sequence 98, Appl
4	170	16.4		16	US-10-741-790-98	Sequence 98, Appl
Ŋ	167.5			70	US-09-766-511B-55	Sequence 55, Appl
9	164.5	15.9	182	o,	US-09-764-870-310	Sequence 310, App
7	164.5			14	US-10-125-540-310	Sequence 310, App
8	163			10	US-09-759-130B-108	Sequence 108, App
6	163			16	US-10-741-790-108	Sequence 108, App
10	191			13	US-10-114-893-22	Sequence 22, Appl
11	160			14	US-10-270-470-2	Sequence 2, Appli
12	159.5			10	US-09-759-130B-83	Sequence 83, Appl
13	159.5			16	US-10-741-790-83	Sequence 83, Appl
14	155			15	US-10-335-009-4	Sequence 4, Appli
7	155			10	US-09-919-039-130	Seguence 130, App

Sequence 10, Appl		Sequence 100, App	Sequence 85, Appl	Sequence 85, Appl	Sequence 340, App	Sequence 486, App	Sequence 340, App	Sequence 486, App	Sequence 11, Appl	Sequence 32, Appl	Sequence 2, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 90, Appl	Sequence 86, Appl	Sequence 86, Appl	Sequence 12, Appl	Sequence 466, App	Sequence 466, App	Sequence 6, Appli	Sequence 1275, Ap	Sequence 110, App	Sequence 110, App	Sequence 302, App	Sequence 302, App	Sequence 5855, Ap	A,	Sequence 836, App
US-10-335-009-10	US-09-759-130B-100	US-10-741-790-100	US-09-759-130B-85	US-10-741-790-85	US-09-764-870-340	US-09-764-870-486	US-10-125-540-340	US-10-125-540-486	US-09-284-320-11	US-10-114-893-32	US-10-088-859-2	US-10-179-528-1	US-10-239-656-3	US-10-239-656-2	US-10-239-656-90	US-09-759-130B-86	US-10-741-790-86	US-10-775-640-12	US-09-764-870-466	US-10-125-540-466	US-09-944-807-6	US-10-296-115-1275	US-09-759-130B-110	US-10-741-790-110	US-09-764-8:70-302	US-10-125-540-302	US-10-106-698-5855	US-09-964-956-67	US-10-072-012-836
15	10	16	10	16	σ	σ	14	14	10	13	14	14	12	12	12	10	16	16	σ	14	6	12	10	16	σ	14	14	12	12
179	138	138	162	162	140	140	140	140	149	149	149	149	133	143	162	187	187	187	94	94	149	146	117	117	119	119	137	124	124
15.0	14.9	14.9	14.9	14.9	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.2	14.2	14.1	14.1	14.0	14.0	13.9	13.9	13.9	13.7	13.7
155	154	154	154	154	153.5	153.5	153.5	153.5	153.5	153.5	153.5	153.5	153	153	153	153	153	153	147.5	147.5	146.5	146	145	145	144.5	144.5	144	142	142
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Sequence 5, Application US/09811367B;
Patent No. US20020155110A1
GENERAL INFORMATION:
APPLICANT: GEMINI SCIENCE, INC.
APPLICANT: Takabashi, No. US20020155110A1uaki
APPLICANT: Takabashi, No. US20020155110A1uaki
APPLICANT: Takabashi, No. US20020155110A1uaki
APPLICANT: Mikayama, Toshifumi
TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (WAPA)
TITLE OF INVENTION: UNMER: US/09/811,367B
CURRENT APPLICATION NUMBER: 2002-03-12
FILE REPERENCE: 021286/0278719
CURRENT APPLICATION NUMBER: 60/190,716
FRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 20
SOCTWARE: Patentin version 3.0
SOFUND NO 5
FRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 20
SOFUND NO 5
FRIOR FILING DATE: 2000-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120
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100.0%; Score 1036; DB 9; Length 188;
Best Local Similarity 100.0%; Pred. No. 2.7e-99;
Matches 188; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-811-367B-5
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APPLICANT: McCarthy, Gean A
APPLICANT: Fraser, Christopher C
APPLICANT: Barnes, Thomas S
APPLICANT: Barnes, Thomas S
APPLICANT: Mackay, Charles R
APPLICANT: Mackay, Charles R
APPLICANT: Mackay, Charles R
APPLICANT: Mackay, Charles R
APPLICANT: Mackay, Revin R
APPLICANT: Mackay, Revin R
APPLICANT: Heiby, Kevin R
APPLICANT: Holtzman, Douglass A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: WEGGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: USES:
TITLE OF INVENTION: USES:
TITLE OF INVENTION: USES:
CURRENT APPLICATION NUMBER: US/10/741,790
CURRENT APPLICATION NUMBER: 2003-12-19
CURRENT FILING DATE: 2003-12-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 SESSWNESRDFCKGKGSTLAIVNTPEKLKFLQDITDAEKYFIGLIYHREEKRWRWINNSV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 MVALGLLTVIL-----MSLLLYQRTLCCGSKGFMCSQC--SRCPNLWMRNGSHCYYFSM 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.4%; Score 170; DB 10; Length 165; 27.3%; Pred. No. 1.8e-09; ive 31; Mismatches 68; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 LSLSILSNSVVQKCGTIHRCGL----HASSCEVALQWICEK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 FNGNVTNQNPNCATI---GLTKTFDAASCDISYRRICEK 162
PRIOR FILING DATE: 2000-01-07
PRIOR PLING DATE: 2000-01-07
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PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 1999-06-14
PRIOR PRILING DATE: 1999-06-14
PRIOR PLING DATE: 1999-06-14
PRIOR PLING DATE: 1999-06-29
PRIOR PLING DATE: 1999-06-29
PRIOR PLING DATE: 1999-06-29
PRIOR PLING DATE: 1999-06-29
PRIOR PLING DATE: 1999-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/503,996
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR PLING DATE: 2000-06-32
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR APPLICATION NUMBER: US 09/420,707
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PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR PRILING DATE: 1999-10-19
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PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR APPLICAT
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PRIOR FILING DATE: 2000-01-07
PRIOR PELING DATE: 2000-04-27
PRIOR PILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/578,063
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Publication No. US20040121396A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-759-130B-98
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US-10-741-790-98
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                                                                                                                                                                                                                                                                                                                         APPLICANT: GENINI SCIENCE, INC.
APPLICANT: Takahashi, No. US2020155110Aluaki
APPLICANT: Takahashi, No. US2020155110Aluaki
APPLICANT: Mikayama, Toshidumi
TITLANT: Mikayama, Toshidumi
TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THEM
FILE REFRENCE: 021286/0278119
CURRENT APPLICATION NUMBER: US/09/811,367B
PRIOR APPLICATION NUMBER: 60/190,716
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: OF DESCRIPTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND CTHER
TITLE OF INVENTION: USES.
TITLE OF INVENTION: USES.
THE REPRESENCE: WPTOO-255-SOMIN
CURRENT APPLICATION NUMBER: US/09/759,130B
CURRENT APPLICATION 1000-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

80.9%; Score 838; DB 9;
Best Local Similarity 80.7%; Pred. No. 9:7e-79;
Matches 151; Conservative 15; Mismatches 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 98, Application US/09759130B Publication No. US20030022279A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                   Sequence 3, Application US/09811367B
Patent No. US20020155110A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barnes, Thomas S
Kirst, Susan J
Mackay, Charles R
Myers, Paul S
Leiby, Kevin R
Wrighton, Nicolas
Goodearl, Andrew
      181 WICEKVLP 188
                                                             181 WICEKVLP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mus musculus
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Farent No. US20020042366A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

ITLE OF INVENTION: NUMBER: US/09/764,870

CURRENT APPLICATION NUMBER: US/09/764,870

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper invMBER OF SEQ ID NOS: 646

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 310
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                                                                                                                                                                                                                                                                                                                                     DB 10; Length 161;
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Anti
FILE REFERENCE: PTZ14C1
CURRENT APPLES: 2002-04-19
CURRENT FILING DATE: 2002-04-19
Prior Application removed - See File Wrapper or Palm
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                                                                                                                                                                                                                                                                                                                                     16.2%; Score 167.5; DB 1
28.7%; Pred. No. 3.2e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 EQCASIVFWKPTGWGWNDVICETRRNSICE 155
                                                                                                                                                                                                                                                                                                                                                                                                              21; Mismatches
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   PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin version 3.1
SEQ ID NO 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 HASSCEVALOWICE 184
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Matches 36; Conserv
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                                                                                                                                                     LENGTH: 161
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APPLICANT: HOLTZMAN, Douglas A
APPLICANT: HOLTZMAN, Douglas A
APPLICANT: KHODADOUST, Mehran M
ITILE OF INVENTION: WOVEL GENES ENCODING PROTEINS HAVING PROGNOSTIC, DIAGNOSTIC, PREV
TITLE OF INVENTION: THERAPEUTIC, AND OTHER USES
FILE REFERENCE: 10147-65
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CURRENT FILING DATE: 2002-05-07
PRIOR PEPLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR PILING DATE: 1999-06-16
PRIOR PILING DATE: 1999-06-16
PRIOR PILING DATE: 1999-06-16
PRIOR PILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/342,364
PRIOR PILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 2000-06-30
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PRIOR FILING DATE: 2000-05-24
PRIOR PLING DATE: 1999-06-14
PRIOR PLING DATE: 1999-06-14
PRIOR PLING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 2000-06-33
PRIOR FILING DATE: 2000-06-33
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
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PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
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APPLICANT: FRASER, Christopher C
APPLICANT: SHARP, John D
APPLICANT: BARNES, Thomas S
APPLICANT: KIRST, Susan J
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WRIGHTON, Nicholas
GOODEARL, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1999-09-10
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 44; Conserv
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US-09-766-511B-55
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APPLICANT:
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ORGANISM: Homo sapiens
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US-09-759-130B-108
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APPLICANT: Goodearl, Andrew
APPLICANT: Goodearl, Andrew
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: USES.
FILE REFERENCE: MPI00-5350MNLM
                                                                                                                                                                                                                                                                                                                                                                                                                                             62 CGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNOGVNL 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                             Query Match
15.9%; Score 164.5; DB 14;
Best Local Similarity 26.9%; Pred. No. 7.7e-09;
Matches 36; Conservative 22; Mismatches 59; I
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CURRENT PELING DATE: 2002-09-16
PRIOR PELING DATE: 2002-09-16
PRIOR PELING DATE: 2000-01-07
PRIOR PELING DATE: 2000-01-07
PRIOR PILING DATE: 2000-04-27
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PRIOR PELING DATE: 1990-06-14
PRIOR PELING DATE: 1990-06-14
PRIOR PELING DATE: 1990-06-19
PRIOR PELING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/596,194
PRIOR PELING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US 09/608,452
PRIOR PELING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR PELING DATE: 2000-06-33
PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR APPLICATION NUMBER: US 09/420,707
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PRIOR PELING DATE: 1999-10-19
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PRIOR APPLICATION NUMBER: US 09/
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Sequence 108, Application US/09759130B
Publication No. US20030022279A1
FEBREAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McCarthy, Sean A
Fraser, Christopher C
Sharp, John D
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Myers, Paul S
Leiby, Kevin R
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Kirst, Susan J
NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 310
LENGTH: 182
                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-10-125-540-310
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LENGTH: 145
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APPLICANT:
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APPLICANT: Mackay, Charles R
APPLICANT: Myers, Paul S
APPLICANT: Leiby, Kevin R
APPLICANT: Leiby, Kevin R
APPLICANT: Wrighton, Nicolas
APPLICANT: Goodearl, Andrew
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: USES.
TITLE OF INVENTION: USES.
                                                                       9
                                                                                                                                                                                                                                            95 DWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGL---RDIDGWRWEDGPALSL 151
                                                                                                                                                                                                                                                                                                       48 SWNESRDFCKGKGSTLAIVNTPEKLKFLQDITDAEKYFIGLIYHREEKRWRWINNSVFNG 107
                                                                                                                         40 MVALGLITVIL----MSL-LLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKR 94
                                                                                                                                                                 -----FCPKDWEFYQARCFFLSTSES
      Length 145;
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                                                                                                                                                                                                                                                                                                                                                                                                    108 NVTNQNFNCATI---GLTKTFDAASCDISYRRICEK 142
                                                                                                                                                                                                                                                                                                                                                               152 SILSNSVVQKCGTIHRCGL----HASSCEVALQWICEK 185
Query Match
15.7%; Score 163; DB 10;
Best Local Similarity 28.5%; Pred. No. 8.4e-09;
Matches 45; Conservative 25; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TILLE COFINENTION: USES:
CURRENT APPLICATION NUMBER: US/10/741,790
CURRENT FILIDE DATE: 2003-12-19
CURRENT FILING DATE: 2003-12-19
PRIOR APPLICATION NUMBER: US 09/479,249
PRIOR FILING DATE: 2000-01-07
PRIOR PELING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 1999-06-14
PRIOR PLING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 1999-06-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-10-10
PRIOR FILING DATE: 1999-10-10
PRIOR FILING DATE: 1999-10-19
NUMBER: OF SEQ ID NOS: 460
SEQ ID NO 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Millennium Pharmaceuticals, Inc. APPLICANT: McCarthy, Sean A APPLICANT: Fraser, Christopher C APPLICANT: Sharp, John D
                                                                                                                                                                        5 MIISGLIVVVLKVVGMTLFLLY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 108, Application US/10741790
Publication No. US20040121396A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barnes, Thomas S
Kirst, Susan J
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; ORGANISM: Homo sapiens
US-10-741-790-108
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APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Garlin-Duckett, McKeough
APPLICANT: Garlin-Fix Kerry S.
APPLICANT: Genetics Institute, Inc.
ITILE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REPERENCE: G1 6000-10A
CURRENT FILING DATE: 2000-04-02
EARLIER APPLICATION NUMBER: 09/413,232
EARLIER PILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 321
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 DWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGL---RDIDGWRWEDGPALSL 151
                                                                             -----FCPKDWEFYQARCFFLSTSES 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 YLVMVALGLITVILMSLL--LYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKR 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 MVALGLILTVIL----MSL-LLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKR 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
  Gaps
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  32;
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Llarity 26.2%; Pred. No. 1.8e-08;
Conservative 27; Mismatches 67; Indels 24
  56; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 FPILGAG-----ECAYLNDKGASSARHYTERKWICSK 176
                                                                                                                                                                                                                            108 NVTNQNQNFNCATI---GLTKTFDAASCDISYRRICEK 142
                                                                                                                                                                                                     152 SILSNSVVQKCGTIHRCGL----HASSCEVALQWICEK 185
  25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chalus, Lionel
APPLICANT: Quan, Ahn B.
APPLICANT: Bates, Blizabeth Ester Mary
APPLICANT: Gorman, Daniel M.
APPLICANT: Saeland, Sem
                                                                                                                                                                                                                                                                                                                                            , Sequence 22, Application US/10114893
, Publication No. US20020193567A1
, GENERAL INFORMATION:
                                                                   Sequence 2, Application US/10270470 Publication No. US20030162955A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jacobs, Kenneth
APPLICANT: MCOSY, JOHN M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa
  45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LaVallie, EdwaPLICANT: Collins-Racie
APPLICANT: Evans, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-10-114-893-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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US-10-114-893-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42;
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US-10-270-470-2
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APPLICANT: HOLICAMAT: DOUGLAS A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: BOGGOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: USES.
TITLE OF INVENTION: USES.
TITLE OF INVENTION: UNRER: US/09/759,130B
CURRENT APPLICATION NUMBER: US/09/759,130B
CURRENT APPLICATION NUMBER: US/09/479,249
PRIOR FILING DATE: 2000-01-07
PRIOR FILING DATE: 2000-01-07
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PRIOR FILING DATE: 2000-01-07
PRIOR FILING DATE: 1099-06-14
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PRIOR FILING DATE: 1090-06-30
APPLICANT: Lebecque, Serge J.E.
APPLICANT: Phillips, Joseph H.
TITLE OF INVENTION: ISOLATED MAMMALIAN MEMBRANE PROTEIN GENES; RELATED REAGENTS: FILE REFERENCE: DX0802QP.
CURRENT APPLICATION NUMBER: US/10/270,470
CURRENT FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 10
SOGTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 162
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Fraser, Christopher C
Sharp, John D
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Myers, Paul S
Leiby, Kevin R
Wrighton, Nicolas
Goodearl, Andrew
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Kirst, Susan J
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Best Local Similarity
Matches 34; Conserv
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Query Match
Best Local Similarity
Matches 47; Conserv
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Matches 36; Conserv
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                                                                                                                                     US-10-741-790-83
                                                                        LENGTH: 188
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US-10-335-009-4
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TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPBUTIC, AND OTHER
TITLE OF INVENTION: USES.
                                                                                                                                                                                                                                                                                                                                                                        71 QC--SRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGE 128
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Best Local Similarity 25.5%; Pred. No. 2.6e-08;
Matches 47; Conservative 31; Mismatches 65; Indels 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 83, Application US/10741790
Publication No. US20040121396A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Fraser, Christopher C
APPLICANT: Sharp, John D
APPLICANT: Sharp, John D
APPLICANT: Kirst, Susan J
APPLICANT: Kirst, Susan J
APPLICANT: Mackay, Charles R
APPLICANT: Myers, Paul S
APPLICANT: Leiby, Kevin R
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CURRENT APPLICATION NUMBER: US/10/741,790
CURRENT FILING DATE: 2003-12-19
FRIOR FILING DATE: 2000-01-07
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-06-30
PRIOR PRIOR DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 09/5033,996
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 1999-10-19
                  NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 83
IRNGTH: 188
TYPE: PRT
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FILE REFERENCE: MPI00-535OMNIM
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Goodearl, Andrew
PRIOR FILING DATE: 1999-10-19
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US-10-741-790-83
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APPLICANT: Boles, Kent S.

TITLE OF INVENTION: LLT USES THEREOF IN IMMUNE SYSTEM MODULATION FILE REPERENCE: 11707-02/469687-7

CURRENT APPLICATION NUMBER: US/10/335,009

PRIOR APPLICATION NUMBER: US/09/475,365

PRIOR APPLICATION NUMBER: US 09/475,365
                                                                                                                                                                                                   DB 16; Length 188;
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                                                                                                                                                                                                                                                 65; Indels
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1 Similarity 25.5%; Pred. No. 2.6e-08,
47; Conservative 31; Mismatches 65
NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 83
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; ENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
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Publication No. US20040001804A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                              40 MVALGLLTVIL----MSLLL
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SOFTWARE: PatentIn version 3.2
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                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919, 039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF EQ ID NOS: 401
SOUTHARE: PERL PROGRAM
SEQ ID NO 130
LENGTH: 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 WK-VKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTLCCGSKGFM--CSQCSRCPNLWW 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 IDGWRWEDGPALSLSILSNSV---VQKCGTIHRCG-LHASSCEVALQWICEKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
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                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
CTHER INFORMATION: Incyte ID No. US20030108871A1 516300CD1
US-09-919-039-130
                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 5,
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1. 'CGTZ_6/Ptodata/2/iaa/5A_COMB.pep:*
2. 'CGTZ_6/Ptodata/2/iaa/5B_COMB.pep:*
3. 'CGTZ_6/Ptodata/2/iaa/6A_COMB.pep:*
4. 'CGTZ_6/Ptodata/2/iaa/6B_COMB.pep:*
5. 'CGTZ_6/Ptodata/2/iaa/PCTTG_COMB.pep:*
6. 'CGTZ_6/Ptodata/2/iaa/PCTTG_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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PCT-US95-04258-5
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US-09-531-056A-23
US-08-722-126A-8
US-08-722-126A-8
US-08-722-126A-8
US-08-722-126A-9
US-08-650-578-2
US-08-650-578-2
US-08-650-578-2
US-08-650-578-2
US-08-113-789-9
US-09-113-789-9
US-09-113-789-9
US-08-122-126A-9
US-08-772-440-11
US-08-772-440-11
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US-09-531-056A-18
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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length: 188
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Perfect
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Sequence 16, Appl Sequence 15, Appl Sequence 23, Appl Sequence 27, Appl Sequence 27, Appl Sequence 2, Appl Sequence 2, Appli Sequence 2, Appli Sequence 14, Appl Sequence 14, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli		(MAFA)
US-08-772-440-16 US-09-531-056A-15 US-08-772-440-23 US-08-772-440-23 US-08-772-440-23 US-08-772-440-14 US-08-731-056A-22 US-08-294-859-2 US-08-294-859-2 US-09-531-056A-21 US-09-535-521-11 US-09-535-521-14 US-09-535-521-17 US-09-535-521-17 US-09-531-056A-21 US-07-833-929A-4 PCT-US92-10344-4	ALIGNMENTS	10 D. MOLECULE ENCODING A MACASSOCIATED ANTIGEN NN-ASSOCIATED ANTIGEN NM-ASSOCIATED ANTIGEN NM-ASSOCIATED ANTIGEN F AMERICA F AMERICA Se #1.0, Version #1.30 8/722,126A US95/04258 EPCHT=1A ON:
24 4 4 4 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6		pplication US/087221 MATION: PECHT, Israel GUTHARANA, Marcelo TAL, Michael UNENTION: PUNCTION- UNCE ADDRESS: SONTHON: PUNCTION- UNITED STATES OF A 19 Seventh Street Schington UNITED STATES OF A 19 Seventh Street SCOOR STATES OF A 19 SEVENTION: PUNCTION- UNITED STATES OF A 19 SEVENTION: PONCY SONTE FORM: FEB Floppy disk TEM FC COMPACTION OF STATES ON NUMBER: PC-DOS/MS SONTES 08-08-08-08-08-08-08-08-08-08-08-08-08-0
		BESULT 1 18-08-722-126A-5 Sequence 5, Application US/087221 Sequence 5, Application US/087221 Ratent No. 603427 GENERAL INFORMATION: APPLICANT: PECHT, Israel APPLICANT: TAL, Michael APPLICANT: TAL, Michael APPLICANT: TAL, Michael TITLE OF INVENTION: FUNCTION- NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS: ADDRESSEE: RROWDY AND NEIMA STATE: D.C. COUNTRY: Washington STATE: D.C. COMPUTER READABLE FORM: MEDIUM TYPE FILOPY disk COMPUTER: BM PC COMPALIBLE COMPUTER: BM PC COMPALIBLE COMPUTER: BM PC COMPALIBLE COMPUTER: BM PC COMPALIBLE COMPUTER: BM PC COMPALIBLE COMPUTER: BM PC COMPALIBLE COMPUTER: BM PC COMPALIBLE COMPUTER: BM PC COMPALIBLE COMPUTER: BM PC COMPALIBLE COMPUTER: BM PC COMPALIBLE COMPUTER: BM PC COMPALIBLE COMPUTER: BAPLICATION DATA: APPLICATION NUMBER: PCT/US9 FILING DATE: 06-APR-1995 FILING DATE: 06-APR-1995 FILING DATE: 06-APR-1995 FILING DATE: 06-APR-1995 FILING DATE: 06-APR-1995 FILING DATE: 08-APR-1995 FILING DAT
135 5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		Sequence 5, Applicat: Sequence 5, Applicat: Sequence 5, Applicat: Sequence 5, Applicat: Sequence 5, Applicat: Sequence 5, Applicat: Sequence 6, G034227 SEGUENCY: SPECITY: SPECITY: STREET: A19 Seguency: CORRESPONDENCE ADD ADDRESSES: BROG STATE: D.C. COMPUTER: D.C. COMPUTER: D.C. COMPUTER: D.C. COMPUTER: D.C. COMPUTER: D.C. COMPUTER: D.C. COMPUTER: D.C. COMPUTER: D.C. COMPUTER: D.C. SOFTWARE: D.C. COMPUTER: D.
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Length 188;

Score 1036; DB 3; Pred. No. 1.3e-105;

100.0%; 100.0%;

Query Match Best Local Similarity

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121 LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQ 180
                                             121 LFQEYVGEDFYWIGLRDIDGWRWEDGFALSLSILSNSVVQKCGTIHRCGLHASSCEVALO 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIG
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                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: PEGCHT, Israel
APPLICANT: GUTHMANN, Marcelo D.
APPLICANT: GUTHMANN, Marcelo D.
APPLICANT: TAL, Michael
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELI
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
NUMBER OF SEQUENCES: 20
CORRESPONDENCES: ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,126A
FT.ING DATE: 08-OCT-1996
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100.0%; Pred. No. 9.7e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C. STREET: 419 Seventh Street N.W., Ste. 300 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 9.7
Mismatches
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APPLICATION NUMBER:
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1L 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D.C. : UNITED STATES OF AMERICA
                                                                                                                                                                                                                                           Sequence 6, Application US/08722126A Patent No. 6034227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION: (202) 628-5197
TELERA: (202) 737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino
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Matches 114; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PE
TELECOMMUNICATION:
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amino acid
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US-08-722-126A-6
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PCT-US95-04258-6
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                                                                                                                                                                                                                  121 LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQ 180
                                                                                                                                                                                                                                           CGGSKGFMCSQCSRCPNLWMRNGSHCYYFSWEKRDWNSSLKFCADKGSHLLTFFDNQGVN 120
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                                                                                                                               CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN
                                           1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
                                                                         1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVWVALGLITVILMSLLLYORTL
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  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A DNA MOLECULE ENCODING A MAST CELL FUNCTION-ASSOCIATED ANTIGEN (MAFA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application PC/TUS9504258
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: A DNA MOLECULE ENCODING A
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEB: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIF: 2004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
ATTORNEY AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
REGISTRATION NUMBER: 25,618
REGISTRATION NUMBER: 25,618
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TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 248633
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 188 amino acids TYPE: amino acid
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Best Local Similarity 100.
Matches 188; Conservative
Matches 188; Conservative
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                                                                                                                                                                                                                                                                                                         181 WICEKVLP 188
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                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
PCT-US95-04258-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US95-04258-5
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                                                                                      75 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLITFPDNQGVNLFQEYVGEDFYWIG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 CPDR#MKYGNHCYYFSVEEKDMNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIG 62
                                              0; Gaps
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    Length 76;
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: PECHT, Israel
APPLICANT: GUTHMANN, Marcelo D.
APPLICANT: GUTHMANN, Maccelo D.
APPLICANT: TL, Michael
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 08-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 16.1%; Score 166.5; DB 3; Best Local Similarity 27.4%; Pred. No. 1.1e-10; Matches 31; Conservative 22; Mismatches 57;
Query Match 26.4%; Score 273; DB 4; Best Local Similarity 59.7%; Pred. No. 1.4e-22; Matches 43; Conservative 14; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C. STREET: 419 Seventh Street N.W., Ste. 300 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 08-0CT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 11 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET I.
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D.C. : UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PECHT=1A
                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08722126A Patent No. 6034227 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PEG
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 amino acids
                                                                                                                                                                                    135 LRDIDGWRWEDG 146
                                                                                                                                                                                                                              63 LRNMSGWRWEDG 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-722-126A-8
                                                                                                                                                                                                                                                                                                                          US-08-722-126A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                     RESULT 6
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APPLICANT: B-1stol-Myers Squibb Company
APPLICANT: B-1stol-Myers Squibb Company
TITLE OF INVENTION: DAM MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUSI
TITLE OF INVENTION: DAM MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUSI
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: DB20 NP
CURRENT APPLICATION NUMBER: US/09/531,056A
CURRENT FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CPNIMMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNGGVNLFQEYVGEDFYWIG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 LRDIDGWRWEDGPALSISILSNSVVQKCGTIHRCGLHASSCEVALQWICEKVLP 188
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                                                                      A DNA MOLECULE ENCODING A MAST CELL FUNCTION-ASSOCIATED ANTIGEN (MAFA)
                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                  STREET: 419 Seventh Street, N.W., Suite 300 CITY: Washington STATE: D.C. STATE: D.C. GODWIRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.8%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PECHT=1 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1594
ATTORNAY AGGENT INFORMATION:
NAME: BROWDY, ROGET L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23, Application US/09531056A Patent No. 6455683
       Sequence 6, Application PC/TUS9504258 GENERAL INFORMATION:
                                                                                                                                                                 BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 25, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT; CRGANISM: Homo sapiens
US-09-531-056A-23
                                              APPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
US-09-531-056A-23
                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US95-04258-6
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Matches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 23
LENGTH: 76
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50 LMSLLLYQRTLCCGSKGFMCSQ----CSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCAD 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:||:
68 MGAHLVVINTEAEQNFITQQINESLSYFLGLSDPQGNGKWQWIDDTPFSQNVRFWHPHEP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 LYELHTYHSSLTCFSEGTMVSEKMMGC--CPNHWKSFGSSCYLLSTKENFWSTSEQNCVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 167;
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; Patent No. 579248
; GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN NUMBER OF ENGURENCE: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
STREET: CA
STREET: CA
STREET: CA
STREET: CA
STREET: CA
STREET: CA
STREET: CA
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STREET: CA
STREET: CA
STREET: CA
                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/772,440
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PATKET, David L.
REGISTRATION NUMBER: 32,165
REGISTRATION NUMBER: 10TD:493
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION OF STO 1D NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
15.3%; Score 158.5; DB 3;
Best Local Similarity 28.6%; Pred. No. 1.3e-09;
Matches 44; Conservative 23; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 NSVVQKCGTI-----HRCGLHASSCEVALQWICE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,095
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0110 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 167 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                     77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-690-095-9
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Patent No. 6046188

GENERAL INFORMATION:
APPLICANT: Arizumi, Kiyoshi
APPLICANT: Takashima, Akira
TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
16.1%; Score 166.5; DB 5; Length 115;
Best Local Similarity 27.4%; Pred. No. 1.1e-10;
Matches 31; Conservative 22; Mismatches 57; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PACTORING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACTORING SYSTEM: PCT/US95/04258
APPLICATION NUMBER: PCT/US95/04258
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: PCT/
REFERENCE/DOCKET NUMBER: PCT/
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                          A DNA MOLECULE ENCODING A MAST CELL
FUNCTION-ASSOCIATED ANTIGEN (MAFA)
                                                                                                                                                                                                                                                                 STREET: 419 Seventh Street, N.W., Suite 300 CITY: Washington
                                                           Sequence 8, Application PC/TUS9504258
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: A DNA MOLECULE F
TITLE OF INVENTION: FUNCTION-ASSOCIA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 115 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 248633
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                          STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: P.O. I
                                                                                                                                                                                                                                                                                                                                                                          20004
                                   PCT-US95-04258-8
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à ď ò Length 179;

Indels

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81 RNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGL---RD 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 WK-VKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTLCCGSKGFM--CSQCSRCPNLWM 80
                                                                                                                                                                                                                      24 WK-VKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTLCCGSKGFM--CSQCSRCPNLWM 80
                                                                                                                                                                                                                                             9 WRLISGTLGIICLS--LMATLGILLKNSFTKLSIEPAFTPGPNIELQKDSDCCSCQEKWV 66
                                                                                                                                                                                                                                                                                                                                                                                                                            138 IDGWRWEDGPALSLSILSNSV---VQKCGTIHRCG-LHASSCEVALQWICEKVL 187
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                                                                                                                             Query Match
15.0%; Score 155; DB 2;
Best Local Similarity 27.0%; Pred. No. 3.5e-09;
Matches 47; Conservative 28; Mismatches 85.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: AL-Young, Janice
APPLICANT: Cocks, Benjamin G.
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
ONNBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE DOCKET NUMBER: PF-0095-1 CIP
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/688,342
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08688342
Patent No. 5871964
GENERAL INFORMATION:
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179 amino acids
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INFORMATION FOR SEQ ID NO:
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                                                            ; MOLECULE TYPE: protein US-08-650-578-2
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Best Local Similarity
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 3174 Port
CITY: Palo Alto
STATE: CA
COUNTRY: US
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STRANDEDNESS: sin
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CLONE: 1098616
                  TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                            24 WK-VKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTLCGGSKGFM--CSQCSRCPNLWM 80
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                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 27.0%; Pred. No. 3.5e-09;
Matches 47; Conservative 28; Mismatches 85; Indels
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APPLICANT: Lopez-Botet, Miguel
APPLICANT: Lopez-Botet, Miguel
APPLICANT: Phillips Jr., Joseph H.
APPLICANT: Lanier, Lewis L.
TITLE OF INVENTION: Purified Mammalian NK Antigens and
TITLE OF INVENTION: Related Reagents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSEE: DNAX Research Institute
I: 901 California Avenue
Palo Alto
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,339
FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/650,578 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5811284
GENERAL INFORMATION:
APPLICANT: Chang, Chiwen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34,090
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
  TELECOMMUNICATION INFORMATION:
                                                              INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                           LENGTH: 179 amino acids
TYPE: amino acid
STRANDEDNESS: single
                       : 415-855-0555
415-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415-496-1200
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                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1098617
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ZIP: 94304-1104
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                         TELEPHONE:
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Length 179;

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125 HTAWLWENGSALSQYLFPSFETFNTKNCIAYNFUALDESCEDKNRYICKQQL 178
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/690,095
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US-08-722-126A-9
; Sequence 9, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                        Sequence 9, Application US/09113789
Patent No. 6034219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PI
TELECOMMUNICATION INFORMATION
TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 179 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                         RESULT 13
US-09-113-789-9
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                                                                                                 81 RNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNOGVNLFQEYVGEDFYWIGL---RD 137
                                                                                                                                                      67 GYRCNCYFISSEQKTWNESRHLCASQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 RNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGL---RD 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 WK-VKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTLCCGSKGFM--CSQCSRCPNLWM 80
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                                                                                                                                                                                                                                                                               125 HTAWLWENGSALSQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQOL 178
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15.0%; Score 155; DB 2; Length 179;
Best Local Similarity 27.0%; Pred. No. 3.5e-09;
Matches 47; Conservative 28; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Cocks, Benjamin G.
APPLICANT: Gocks, Benjamin G.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF-0095-1 CIP
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SOFTWARE: FASKEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/113,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/688,342
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09113788
Patent No. 5969104
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ZIE: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
TANDIUM TYPE: Diskette
TOWNTER: IBM COMPAtible
DOS
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INFORMATION FOR SEQ ID NO: 3:
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ATTORNEY/AGENT INFORMATION:
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
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MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIBRARY: GenBank
CLONE: 1098616
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STATE: C
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-09-113-788-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 GYRCNCYFISSEQKTWNESRHLCASQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEE 124
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GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
ITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STRET: 3174 Porter Drive
CITY: Palo Alto
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186 VL 187
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             APPLICANT: GUTHMANN, MATCELO D.
APPLICANT: TAL, Michael
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                COMPUTER KEADABLE FORM:
MEDIUM TYPE: FIDEPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,126A
FILING DATE: 08-OCT-1996
CLASSIFTCATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: PECHT=1A
TELECOMMUNICATION INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: PECHT=1A
TELECOMMUNICATION INFORMATION:
MATTORNEY/AGENT NUMBER: PECHT=1A
                                                                                                                                                   ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
                                                                                                                                                                                                                                           UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application PC/TUS9504258 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-5328
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 amino acids
PECHT, Israel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                           ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                     STREET: 419 Seven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington
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COUNTRY: U
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PCT-US95-04258-9
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APPLICANT:
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Best Local 9
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61 IGLRYTLPDMN-WKWINGSTINSDVLKITGDTENDSCAAISGDKVTFESCNSDNRWICQK 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 IGLR----DIDGWRWEDGPALS---LSILSNSVVQKCGTIHRCGLHASSCEVALQWICEK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CPQDWLSHRDKCFHVSQVSNTWEEGLVDCDGKGATLMLIQDQEELRFLLDSIKEKYNSFW 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.8%; Score 153; DB 5; Length 122; 27.9%; Pred. No. 3.5e-09;
                                                                                        CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04258

FILING DATE: 06-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 109257

FILING DATE: 08-APR-1994

ATTORNEY/AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: 25.618

REFERENCE/DOCKET NUMBER: PECHT=1 PCT

TELECHMONICATION INFORMATION:

TELECHMONICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22; Mismatches
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                                                                          PC-DOS/MS-DOS
                   E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 27.9%
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
COMPUTER READABLE FORM:
                                                 COMPUTER: IBM PC OPERATING SYSTEM:
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 10, 2004, 16:11:32; Search time 32.7823 Seconds (without alignments) 1819.059 Million cell updates/sec Run on:

US-09-811-367B-1 1023 Perfect score:

1 MIDSVIYSMLELPTATQAQN......GLQASSCEVPLHGVCKKVRL 189

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

Sequence:

Title:

residues 1017041 seqs, 315518202 Searched:

1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SPTREMBL 25:* Database :

sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:* sp_vertebrate:*
sp_unclassified:* sp_rvirus:*
sp_bacteriap:* sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:* rodent:* sp virus:* sp_plant:* 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

			Description	043198 homo sapien	075613 homo sapien	homod	088713 mus musculu	064335 rattus norv	Ognzez homo sanien	O9nzsl homo sapien	0802s8 gallus gall	09d403 mis misculii	OsmiO5 macaca fasc	09wu32 mus musculu	054872 rattus norv	O8spx1 sus scrofa		012918 homo sanien	Q8mjh7 pongo pygma
SUMMARIES			Ωï	043198	075613	Ф96Е93	088713	064335	C9NZS2	Q9NZS1	080258	Q9D403	OBMI 05	Q9WU3.2	054872	Q8SPX1	O9MZK3	012918	овмлн7
			BB	4	4	4	11	11	4	4	13	11	9	Π	11	ø	9	4	9
			Match Length DB	189	189	195	188	188	231	181	200	275	231	227	231	200	231	225	233
	οķο	Query	Match	100.0	98.4	97.2	53.6	51.4	22.1	22.0	21.7	21.5	21.4	20.5	20.5	20.0	19.7	19.6	19.6
			Score	1023	1007	994	548.5	525.5	226	225	222	219.5	219	210	210	205	201.5	201	201
		Result	No.	г	2	m	4	Ŋ	9	7	89	σ	10	11	12	13	14	15	16

Q8mjh6 pongo pygma Q8bhh6 mus musculu Q9dk88 macaca mula Q9dk76 mus musculu Q8dvi21 mus musculu Q8mji0 pongo pygma Q5mym6 par troglod O54709 mus musculu Q9mzk2 macaca mula Q9mzk1 macaca mula Q9zz202 mus musculu Q9mzk1 macaca mula Q9zz202 mus musculu Q9xz48 oryctolagus Q91zw9 mus musculu Q8mjh5 pongo pygma Q8mjh5 pongo pygma Q8mjh8 pongo pygma Q90636 gallus gall P79391 bos taurus Q90636 gallus gall Q9vu31 mus musculu Q9wu31 mus musculu Q9wu31 mus musculu Q9wu31 mus musculu Q9wu31 mus musculu Q9wu31 mus musculu Q9wu31 mus musculu Q9wu31 mus musculu Q9wu31 mus musculu	054871 rattus norv Q956mg1 bos taurus Q61973 mus musculu Q8mjil pongo pygma Q8mjil pongo pygma Q8mhy8 pongo pygma Q8mjh0 pongo pygma
	0 11 054871 0 0 12 054871 7 11 061973 9 08MJT3 9 6 Q8MJT0 6 6 Q8MJH0
19.6 19.5 19.5 19.5 19.5 19.5 19.5 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0	18.7 23 18.6 19 18.6 22 18.6 23 18.5 17 18.5 17
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ALIGNMENTS

RESULT 1

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TISSUE=Lung;

W MEDLINE-98438735; PubMed=9765598;

W Laners M.-Lanent.A.G., Williams D.H.;

Laners M.-Lanent.A.G., Williams D.H.;

Laners M.-Lanent.A.G., Williams D.H.;

Laners M.-Laners M.-Lanent.A.G., Williams D.H.;

Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners M.-Laners 
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Eukaryota, Metazona, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SEQUENCE 189 AA; 21079 MW; 15E042AD40B2B4F6 CRC64;
                                                                                                                                                      Last sequence update)
Last annotation update)
                                            189 AA.
                                                                     043198;
01-070-1998 (TrEMBLrel. 06, Created)
01-070N-1998 (TrEMBLrel. 06, Last sequer
01-070N-2003 (TrEMBLrel. 24, Last annote.
Mast cell function-associated antigen.
                                        PRT;
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                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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9 1 MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL

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SEQUENCE FROM N.A.

Hanke T., Corral L., Vance R.E., Raulet D.H.;

Hanke T., Corral L., Vance R.E., Raulet D.H.;

Hanke T., Corral L., Vance R.E., Raulet D.H.;

"Exl antigen, the mouse homolog of the rat '$1', is a lectin-like type of the mouse bandles of the rat '$1', is a lectin-like type of "Exl antigen, the mouse homolog of the rat '$1', is a lectin-like type of "Exl antigen, the mouse homolog of the rat '$1', is a lectin-like type of "Exl antigen, Tannembrane receptor expressed by natural killer cells.";

EMBL, AR091359; AAC32200.1; -

BERI, AR091358; AAD3170.1; -

REMBL, AR091358; AAD3170.1; -

REMBL, AR003358; AAD3170.1; -

PROSITE; PSS0041; C_IYPE_LECTIN_2: 1.
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                                                                                                            LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL
CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS
                                                                                        LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL
                                        COGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS
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                                                                                                                                                                                                                                                                                                                                                                                                     Butcher S., Arney K.L., Cook G.P.; "MARP-L" an ITIM-containing receptor encoded by the human NK cell complex and expressed by basophils and NK cells."; Eur. J. Immunol. 28:0-0(1998).
                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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189 AA: 21206 MW; FA9023F1523656A8 CRC64;
                                                                                                                                                                                                                                                    01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ITIM-Containing receptor MAFA-L.
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                                                                                                                                                                                                                                     189 AA
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                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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STRAIR=CB-17 SCID;
MEDLINE=99771194; PubMed=9862378;
Hanke T., Corral L., Vance R.E., Raulet D.H.;
Hanke T., Corral L., Vance R.E., Raulet D.H.;
"2F1 antigen, the mouse homolog of the rat '$1', is a lectin-like type II transmembrane receptor expressed by natural killer cells.";
Eur. J. Immunol. 28:4409-4417(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS
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01-NOV-1999 (TrEMBLrel. 11, Last sequence update)
01-ACC-1999 (TrEMBLrel. 11, Last sequence update)
01-OCC-2003 (TrEMBLrel. 25, Last annotation update)
Mast cell function-associated antigen 2F1 (MAFA) (Killer cell lectin-like receptor G1).

KIRG1 OR MAFA.

Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                          member
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                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OECT-2003 (TrEMBLrel. 25, Last amotation update)
Similar to killer cell lectin-like receptor subfamily G,
                                                                                                                                                                                                                                                                                             TISSUE=Bone marrow;
Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 AA; 21831 MW; 178EE98E08EEC473 CRC64;
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Genew, HGNC:6380; KLRG1.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0005529; F:sugar binding; IEA.
GO; GO:0007157; P:heterophilic cell adhesion; IEA.
InterPro; IPR001364; Lectin_C.
Ffam; PR00059, lectin_C: 1...
SWART; SW00054; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.2%; Score 994; DB 4; I
98.4%; Pred. No. 1.2e-101;
cive 1; Mismatches 2;
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195 AA
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PRT;
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PRELIMINARY;
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CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS 120
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                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:13342; KLRF1.

GO; GO:0005887; C:integral to plasma membrane; TAS.

GO; GO:0004888; F:transmembrane receptor activity; TAS.

GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . ; TAS.

GO; GO:0007166; P:cell surface receptor linked signal transdu. . ; TAS.
                                                                                                                                                                                                                                                                                                                                                        1 MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL
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Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kucherlapati R.,
Fernandez-Ruiz E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Human KLRRI, a novel member of the killer cell lectin-like receptor gene family: molecular characterization, genomic structure, physical mapping to the NK gene complex and expression analysis.";

Eur. J. Immunol. 30:568-576(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vitale M., Falco M., Castriconi R., Parolini S., Zambello R., Semenzato G., Blassoni R., Bottino C., Moretta L., Moretta A.; "Identification of NKp80, a novel triggering molecule expressed by human natural killer Cells.";
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                      51.4%; Score 525.5; DB 11; Length 188; 53.5%; Pred. No. 7.2e-50; ive 29; Mismatches 57; Indels 1;
                                                                                                                                                                                                        PROSITE; PSS0041; C_TYPE_LECTIN_2; 1.
SEQUENCE 188 AA; 21356 MW; 2CC8032D4D020B15 CRC64;
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24, Last annotation update)
(Activating coreceptor NKp80)
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                     EMEL, X97193; CAA65829.1; JOINED.
EMBL, X97194; CAA65829.1; JOINED.
EMBL, X97195; CAA65829.1; JOINED.
EMBL, X79195; CAA65829.1; JOINED.
FIRE, IS9421; IS9421; -.
GO; GO:0005529; F:sugar binding; IEA.
InterPro; IPR001304; Lectin_C.
Féan; PF00059; lectin_C; I.
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MEDLINE-21150889; PubMed-11265639;
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EMBL; AF175206; AAF37804.1; --
EMBL; AJ305370; CAC29425.1; --
        CAA65829.1; JOINED.
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                                                                                                                                                                                                                                                                                          Local Similarity
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      EMBL; X97192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNGCVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL 180
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                                                                                              STRAIN=129/SvevTACfBr; TISSUB=Spleen,
MEDLINB=21115136; PubMed=11220622;
Woehringer D., Kaufmann M., Pircher H.;
"Genomic structure, alternative splicing, and physical mapping of the killer cell lectin-like receptor Gl gene (KLRG1), the mouse homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A.

MEDLINE=96016176; PubMed=7568140;
Guthmann M.D., Tal M., Pecht I.;
Guthmann M.D., Tal M., Pecht I.;
another C-type lectin.";
Proc. Natl. Acad. Sci. U.S.A. 92:9397-9401(1995).

EMBL; X97191; CAA65829.1; -.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56; Indels
                                        Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=SPRAGUE DAWLEY; TISSUE=Testis;
Bocek Jr P., Guthmann M.D., Pecht I.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 AA; 21396 MW; 876336802EA134F1 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                      MGD; MGI:11355294; KIRGI...,
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0005529; F:sugar binding; IEA.
GO; GO:0007157; P:heterophilic cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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                                                                                                                                                                                                      of MAFA.";
Immunogenetics 52:206-211(2001).
                                                                                                                                                                                                                                             EMBL; AF097357; AAD03718.1; -...
EMBL; AJ010751; CAA09342.1; -..
EMBL; AF317727; AAK40082.1; -.
                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001304; Lectin_C.
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SEQUENCE OF 2-188 FROM N.A.
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les 104; Conservative
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01-NOV-1996 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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                                                                                 SEQUENCE FROM N.A.
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149 IKGPAKENSCAAIKESKIFSETCSSVFKWICQ 180
                                                                                       01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
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SLCHLHKHWVCSR 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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01-JUN-2001 (TrEMBLrel
01-OCT-2003 (TrEMBLrel
4933425816Rik protein.
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nes 53; Conserve
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                  NCBL_TaxID=9031;
                                                                                                                        C-type lectin.
Y-LEC2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                              130 -FCWIGLRNNS---GWRWEDGSPLNFSRISSNSFVQ-----TCGAINKNGLQASSCEVP 179
                                                                                                                                                                                                                                            44 GLLTAVLLSVLLYQWILCQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFC 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 LARDSHLLVITDNQEMSLLQVFLSEA-FCWIGLRNNS---GWRWEDGSPLNFSRISSNSF 159
                                                                                                                              74
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                                                                                                                                                                              ----CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEA
                                                                                                                              SNYSTCASCPS
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EMBL; AF175207; AAF37805.1; -.
GO; GO:0016020; C:membrane; TAS.
GO; GO:0016020; C:membrane; TAS.
GO; GO:0010620; Lectin.C.
Ffam; PF00059; lectin.C.
SWART; SM00034; CLECT; 1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                      48;
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                                                                             Length 231;
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                                                                                                     Indels
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                                                     26562 MW; A2F7BE6D4341AFDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Lectin-like receptor F1, splice variant 1 KLRF1-s1.
KLRF1.
                                                                           22.1%; Score 226; DB 4; L
31.2%; Pred. No. 1.2e-16;
live 27; Mismatches 53;
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Pred. No. 1.1e-16;
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                                                                                                                                                                                                                                                                                                                                                                   181 AA.
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Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                              44 GLLTAVLLSVLLY--QWIL--CQG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=20135860; PubMed=10671213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.0%;
                                                                        Query Match 22.1%;
Best Local Similarity 31.2%
Matches 58; Conservative
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                                                                                                                                                                                                                                                                              180 LHGVCK 185
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                                                     231 AA;
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                                         Receptor.
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---SCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQ 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMSLLQVFLSEAFCWIGL---RNNSGWRWEDGSPL-NFSRISSNSFVQTCGAINKNGLQA 173
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                                                                                                                                                                                                                                                                                                                                                                                  Kalser P.;
"Analysis of part of the chicken Rfp-Y region reveals two novel lectin genes, the first complete genemic sequence of a class I alpha-chain gene, a truncated class II beta-chain gene, and a large CR1 repeat."; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, A277927, CAD61336.1; -.
GO, GO:0007157; P:sugar binding; IEA.
GO; GO:0007157; P:heterophilic cell adhesion; IEA.

InterPro; IPR002353; AntifreezeII.

InterPro; IPR01304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 GPQQKS----SSSKPSCSC-----LVAITLGLLTAVLLSVLLYQWILCQGSNY
                                                                                                                                              Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Rogers S., Shaw I., Ross N., Nair V., Rothwell L., Kaufman J.,
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                         Last sequence update)
Last annotation update)
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Last annotation update)
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27.5%; Pred. No. 2.7e-16;
iive 31; Mismatches 67;
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PRINTS; PR00356; ANTIFREEZEII.
SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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IEA
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                                                                                            PROSITE; PS50041; C TYPE LECTIN 2; 1.
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Eur. J. Immunol. 29.755-761(1999).
EMBL; AR109784; AAD24970.1;
GO; GO:0004872; F:receptor activity;
GO; GO:0005529; F:sugar binding; IEA.
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        EMBL; AJ426430; CAD19994.1;
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                                                                                                                                                                        Local Similarity 30.28
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CQ 230
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                                                                                                                 Receptor.
                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                           184
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                                                                                                                                                           Query Match
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                        Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Anadawa K., Izawa M., Nishi K., Kiyosawa H., Kodoo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito T., Bato T., Saito T., Saito T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Kuell P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Saki K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Borimin L., Boifelli D., Bojunga N., Carninci P., de Bonaldo M.F., Bronstein M.J., Bult C., Pletcher C., Fujita M., Gariboldi M., Bronstein M.J., Bult C., Pletcher C., Fujita M., Gariboldi M., Horons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nackone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sabaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.; Ang K., Hayashizaki Y.; Ang Suzuki H., Rohtsuki S., Nature 409:885-69(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 TCASCPSCPDRWMKYGNHCYYFSV-EEKDWNSSLEFCLARDSHLLVITDNQEMSLL--QV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 FLSEAFCWIGLR-NNSG--WRWEDGS-----PLNFSRISSNSFVQTCGAINKNGLQASSC 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 TQAQNDYGPQQK--SSSSKPSCSCLVAITL-GLLTAVL----LSVLLYQWILCQGSNYS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             th 21.5%; Score 219.5; DB 11; Length 275; Similarity 31.6%; Pred. No. 7.5e-16; 60; Conservative 34; Mismatches 73; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Macaca fascicularis NK cell and receptors.";
Submitted (DRC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                C_TYPE LECTIN 2; 1.
; 31360 MW; C9792BA25CBB5CC2 CRC64;
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Last annotation update)
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MGD; WGI:1918433; 4933425B16Rik.
GG; GO:0005529; F:sugar binding; IEA.
InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
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                MEDLINE=21085660; PubMed=11217851;
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01-OCT-2002 (TrEMBLrel. 22,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255 RAEIPWICEK 264
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Biassoni R.;
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Best Local Similarity
Matches 60; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                              275 AA;
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01-OCT-2003
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75 ----CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEA 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 DQTVLCQSEWLKYRGKCYWFSNEMKSWSDSYVYCLERKSHLLIIQDELEMAFIQKNLRQS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Lohwasser S., Hande P., Mager D.L., Takei F.;
"Cloning of murine NKG2A, B and C: second family of C-type lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.4%; Score 219; DB 6; Length 231; 30.2%; Pred. No. 6.9e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 AA; 26710 MW; 403C79CA6883C1E7 CRC64;
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Last annotation update)
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27.1%; Pred. No. 6.7e-15;
... Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 AA.
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GO; GO:0004872; F:receptor activity; IEA. GO; GO:0005529; F:sugar binding; IEA. InterPro; IPR001304; Lectin_C. Pfam; PF00059; lectin_C; 1. SMART; SM00034; CLECT; 1.
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66 YSTCAS --- CPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQE-MSL 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 LQVFLSEAFCWIGLRNNSG--WRWEDGSPLN--FSRISSNSFVQTCGAINKNGLQASSCE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 PTATQAQNDYGP----QQKSSSSKP-SCSC--LVAITLGLLTAVLLSVLLYQWILCQGSN 65
                                                                                                 Yim D., Sotiriadis J., Kim K.-S., Shin S.-C., Jie H.-B., Rothschild M.F., Kim Y.B., "Molecular cloning, expression pattern, and chromosomal mapping of pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 PNRGQPSNATGPHFATHHEGSLQVPIPCAVNVVFITVLIIALIALSVGQYN---CPGQY
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B,
  Euteleostomi;
Sus.
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MEDLINE=20322487; PubMed=10866118;
LaBonte M.L., Levy D.B., Letvin N.L.;
"Characterization of thesus monkey CD94/NKG2 family members and identification of novel transmembrane-deleted forms of NKG2-A, E
                                                                                                                                                                                                                                                                                                                                                                                                                 22;
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                                                                                                                                                                               Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF444233; AAL91546.1; -.
EMBL; AF444233; AAL91546.1; -.
EQ; GO:0005529; Fsugar binding; IEA.
InterPro; IRR00130; Lectin_C.
Pfam; PF00059; lectin_c; 1.
PROSITE; SM00034; CLECT; 1.
PROSITE; PS05041; C TYPE LECT; 1.
SEQUENCE 200 AA; 22257 MW; G5589767E163A57C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenetics 51:496-499 (2000).

EMBL; AF19037; AAF74533.1; -.

HSSP; P22897; IEGG.

GO; GO;0005229; F:sugar binding; IEA.

InterPro; IPR001304; Lectin C.

Pfam; PR00034; CLECT; 1.

PROSITE; PS50041; CTYPE LECTIN 2; 1.

SRQUENCE 231 AA; 26107 MW; GD0307ABE0262DBD CRC64;
  Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                      20.0%; Score 205; DB 6; Le
29.6%; Pred. No. 2.1e-14;
tive 27; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
19.7%; Score 201.5; DB 6;
Best Local Similarity 29.8%; Pred. No. 6e-14;
Matches 59; Conservative 30; Mismatches 92;
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                                                                                                                                                                                                                                                                                                                                                                                                                    56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 VPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 KNLHWICSK 197
                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9823;
                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9544;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 PSQEQTRICRDCHCKGFPSPPEKLIAGTLGFISFVLIVAVVVITTVATPYTETKAQINSS 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 ST----CASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 QVFLSEAFCWIGLRNNS---GWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVP 179
                                             CYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIG-LRNNSG--WR 142
                                                                       KGFPSPPEKLIAGTLGLICFVLIVAVVVITTVATPYINYTLSSAQPCPHCPKEWISYSHN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 MTRIYQARPCIRCPDDWISYSHNCYYISVERKSWNDGLISCISKNCSLLHIDSEEEQAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 PQQKSSSSKPSCSC-----YQWILLGLLTAVLLSVLL-----YQWILCQGSNY
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=F344;
MEDLINE=98180346; PubMed=9521051;
Berg S.F., Dissen E., Westgaard I.H., Fossum S.;
"Molecular characterization of two genes in the rat homologous to
human NKG2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
                                                                                                                             143 WEDGSPLNFSRISSNSFVQ-----TCGAINKNGLQASSCEVPLHGVCK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 231;
                                                                                                                                                     81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 231 AA; 26335 MW; FF2AE6D33EF2CE99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Type II membrane protein CD69.
Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation updat. Natural killer cell protein group 2-A (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.5%; Score 210; DB 11; 29.0%; Pred, No. 6.9e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eur. J. Immunol. 28:444-450(1998).
EMBL, AP021356, AA040050.1; -.
GO, GO:0005529, F:sugar binding; IEA.
InterPro; IPR002353; Antifreezell.
InterPro; IPR00394; Lectin.C.
PRIMTS; PR00059; lectin.C; 1.
PRIMTS; PR00059; lectin.C; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                    Created)
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(TrEMBLrel. 06, 1
(TrEMBLrel. 25, 1
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                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221 HPYVCK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Q8SPX1

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RESULT 13 Q8SPX1

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:|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| 
                                                                                                                                                                                        LC---QGSNYS-----TCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHL 110
                                                                                                                                                                                                                                                                                                                                                                       LVITDNOEMSLLQVFLSEAFCWIGL-RNNSGWRWEDGSPLNFSRISSNS--FVQTCGAIN 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 LSIDNEEEMKFLTAILPSS--WIGVFRNSSHHPWVTINGLTFKHEIKNSDNAEHNCAMLH 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90
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TDSVIYSMLELPTATQAQNDYGPQQ--KSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWI
                                                                   (i) ESQUENCE FROM N.A.

X MEDLINE=94358407, PubMed=8077657;
X MEDLINE=94358407, PubMed=8077657;
X MEDLINE=94358407, PubMed=8077657;
X Lanier L.L., Chang C., Phillips J.H.;
I L. Chang C., Phillips J.H.;
X Superfamily expressed by a subset of NK and T lymphocytes.";
J. Immunol. 153:241-2428 [1594].
EMBL; U11276; AAA21605.1; -.
EMBL; U11276; AAA21605.1; -.
EMBL; U11276; AAA21605.1; -.
EMBL; U11276; AAA21605.1; -.
EMBL; U11276; AAA21605.1; -.
EMBSP; POS140; ZAPR.
R GO; GO:00055886; C:plasma membrane; TAS.
R GO; GO:00055886; C:plasma membrane; TAS.
R GO; GO:0007166; P:cetl surface receptor activity; TAS.
R GO; GO:0007166; P:cetl surface receptor linked signal transdu. .; TAR INTERPRO SIGNO SIGNAL CLECT; I.
EMBREY; SMO034; CLECT; I.
EMBREY; SMO034; CLECT; II.
EMBREY; SMO034; CLECT; II.
EMBREY; SMO034; CLECT; II.
EMBREY; SMO034; CLECT; II.
EMBREY; SMO034; CLECT; II.
EMBREY; SMO034; CLECT; II.
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Mammalia; Butheria; Primates; Catarrhini; Hominicae; Homo.
NCBI_TaxID=9606;
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